

FIG. 1

Bovine cDNA	1	Met	His	Ser	Asp	5	Cys	Ile	Phe	Lys	Lys	10	Glu	Gln
		*	*	*	*		*	*	*	*	*		*	*
Purified bovine Sample		Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln		
		15				20						25		
		Ala	Met	Cys	Leu	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu
		*	*	*	*	*	*	*	*	*	*	*	*	*
		Ala	Met	Cys	Leu	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu
		Gly	Leu	Asn	Asp									
		*	*	*	*									
		Gly	Leu	Asn	Asp									

FIG. 4

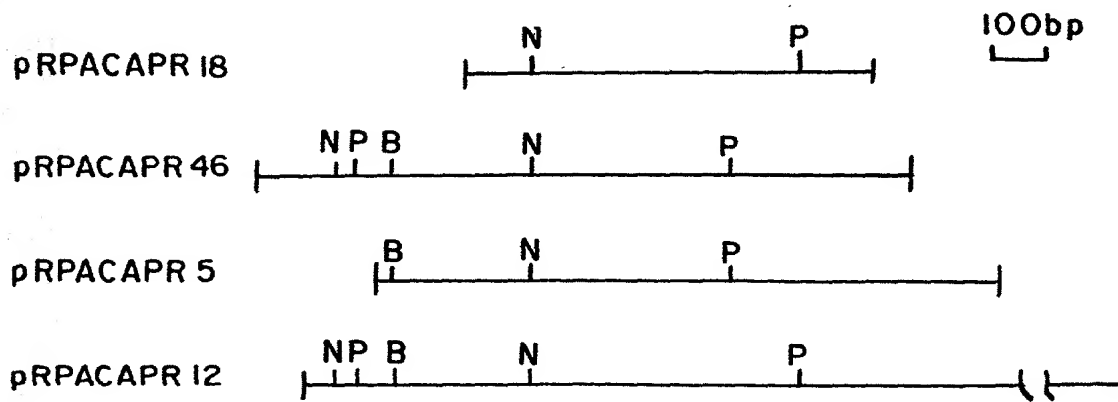


FIG. 6

TGGCCTGCAC	CCCACCCCCC	AGCCTGCGAA	GACGGGGGGA	GGCGGTGGTC	GGTCGCCTCC	60
CTCCTGCCCC	CGGCCTGGCT	TCGCGGTGGA	GGCGGTGCCT	CTCCGGCAAG	GCAGACCAGG	120
CTGGGCGGAC	GCGCGGCGCG	GGGCGGGCTA	GGGAAGGCCG	GGGGCCTCGC	GCTCGGGCCC	180
CGGGCGGGCA	CTGACAGCGG	CGGCGGCGGC	GGCAGCGGCT	CCAAGGCGAG	CGTGGTCCCC	240
GCGTGCGCAC	AAGCTCGCCG	CCGCGCAGGG	ACCCACGGAC	ACCGGCGCCG	GGCGGACACA	300
CAGACGCGGA	GATCGGGCTC	TACGCGCGCT	ACTCAGCGCA	CGAGCTCCCC	ATCCCTGGGC	360
GGAGCGGGGC	GCGGACTCGC	CGCTGCGCGC	CCTCCCCGCG	GAGTCTGCCC	CGGGCAGACC	420
CGCAGCCCGC	GGCCCCGCCG	CGAGGCCCT	GGGTGAGCAG	CCTGTAGACA	CCTGGGGTTG	480
AGCAGTGGCG	GCTGTGA	ATG AGA GGC GGG CGG CAC TGG CCC GAG CCG CCT				530
		Met Arg Gly Gly Arg His Trp Pro Glu Pro Pro				
	1		5		10	

TGC AGG CTG AGA AGC GTC ATG GCC AGC ATC GCG CAG GTC TCC CTG GCT	578
Cys Arg Leu Arg Ser Val Met Ala Ser Ile Ala Gln Val Ser Leu Ala	
15 20 25	

GCT CTC CTC CTG CTG CCT ATG GCC ACC GCC ATG CAT TCC GAC TGC ATC	626
Ala Leu Leu Leu Leu Pro Met Ala Thr Ala Met His Ser Asp Cys Ile	
30 35 40	

TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GTG AAT	674
Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Val Asn	
45 50 55	

GAC CTG ATG GGC TTG AAT GAC TCC TCC CCA GGG TGC CCT GGG ATG TGG	722
Asp Leu Met Gly Leu Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp	
60 65 70 75	

GAC AAC ATC ACG TGT TGG AAG CCC GCC CAC GTG GGT GAG ATG GTC CTG	770
Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu	
80 85 90	

GTC AGT TGC CCT GAA CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG	818
Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp	
95 100 105	

GAG ACG GAA ACC ATC GGA GAG TTC GGT TTT GCA GAC AGT AAA TCC TTG	866
Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe Ala Asp Ser Lys Ser Leu	
110 115 120	

GAT CTC TCA GAC ATG AGG GTG GTG AGC CGG AAT TGC ACG GAG GAT GGA	914
Asp Leu Ser Asp Met Arg Val Val Ser Arg Asn Cys Thr Glu Asp Gly	
125 130 135	

TGG TCA GAG CCA TTC CCT CAT TAT TTC GAT GCC TGT GGG TTT GAG GAG	962
Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Glu Glu	
140 145 150 155	

TAC GAA TCT GAG ACT GGG GAC CAG GAT TAC TAC TAC CTG TCA GTG AAG	1010
Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys	
160 165 170	

FIG. 2A

GCC	CTG	TAC	ACA	GTT	GGC	TAC	AGC	ACG	TCC	CTC	GTC	ACC	CTC	ACC	ACT	1058
Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	Leu	Val	Thr	Leu	Thr	Thr	
			175					180					185			
GCC	ATG	GTC	ATC	CTG	TGT	CGT	TTC	CGG	AAG	CTG	CAC	TGC	ACC	CGC	AAC	1106
Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	Leu	His	Cys	Thr	Arg	Asn	
		190					195					200				
TTC	ATC	CAC	ATG	AAC	CTC	TTC	GTG	TCG	TTT	ATG	CTG	AGG	GCC	ATC	TCC	1154
Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	Ala	Ile	Ser	
	205					210					215					
GTC	TTC	ATC	AAA	GAC	TGG	ATC	CTC	TAT	GCT	GAG	CAG	GAC	AGC	AAT	CAC	1202
Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	Glu	Gln	Asp	Ser	Asn	His	
	220				225					230					235	
TGC	TTT	GTC	TCC	ACT	GTG	GAA	TGC	AAG	GCT	GTG	ATG	GTT	TTC	TTC	CAC	1250
Cys	Phe	Val	Ser	Thr	Val	Glu	Cys	Lys	Ala	Val	Met	Val	Phe	Phe	His	
				240					245					250		
TAC	TGT	GTT	GTA	TCC	AAC	TAC	TTC	TGG	CTG	TTC	ATC	GAG	GGC	CTG	TAT	1298
Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu	Phe	Ile	Glu	Gly	Leu	Tyr	
			255					260					265			
CTC	TTC	ACC	CTG	CTG	GTG	GAG	ACC	TTC	TTC	CCC	GAG	AGG	AGA	TAT	TTC	1346
Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe	Pro	Glu	Arg	Arg	Tyr	Phe	
		270					275					280				
TAC	TGG	TAC	ATC	ATC	ATT	GGC	TGG	GGG	ACA	CCA	ACT	GTG	TGT	GTG	TCT	1394
Tyr	Trp	Tyr	Ile	Ile	Ile	Gly	Trp	Gly	Thr	Pro	Thr	Val	Cys	Val	Ser	
	285					290					295					
GTG	TGG	GCT	ATG	CTG	AGG	CTC	TAC	TTC	GAT	GAC	ACA	GGC	TGC	TGG	GAT	1442
Val	Trp	Ala	Met	Leu	Arg	Leu	Tyr	Phe	Asp	Asp	Thr	Gly	Cys	Trp	Asp	
	300				305			Δ		310					315	
ATG	AAT	GAC	AAC	ACG	GCT	CTG	TGG	TGG	GTG	ATC	AAA	GGC	CCT	GTA	GTT	1490
Met	Asn	Asp	Asn	Thr	Ala	Leu	Trp	Trp	Val	Ile	Lys	Gly	Pro	Val	Val	
				320					325					330		
GGC	TCC	ATA	ATG	GTT	AAT	TTT	GTG	CTC	TTC	ATC	GGC	ATC	ATT	GTC	ATC	1538
Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe	Ile	Gly	Ile	Ile	Val	Ile	
			335					340					345			
CTT	GTG	CAG	AAA	CTT	CAG	TCT	CCA	GAC	ATG	GGA	GGC	AAC	GAG	TCC	AGC	1586
Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met	Gly	Gly	Asn	Glu	Ser	Ser	
		350					355					360				
ATC	TAC	TTC	AGC	TGC	GTG	CAG	AAA	TGC	TAC	TGC	AAG	CCA	CAG	CGG	GCT	1634
Ile	Tyr	Phe	Ser	Cys	Val	Gln	Lys	Cys	Tyr	Cys	Lys	Pro	Gln	Arg	Ala	
	365					370					375					
CAG	CAG	CAC	TCT	TGC	AAG	ATG	TCA	GAA	CTG	TCC	ACC	ATT	ACT	CTA	CGG	1682
Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr	Ile	Thr	Leu	Arg	
												▽				

FIG. 2B

380	385	390	395	
CTC GCC AGG TCC ACC TTG CTG CTC ATC CCA CTC TTT GGA ATC CAC TAC				1730
Leu Ala Arg Ser Thr	Leu Leu Leu Ile	Pro Leu Phe Gly	Ile His Tyr	
	400	405	410	
ACT GTC TTT GCT TTC TCC CCG GAG AAC GTC AGC AAG AGG GAG AGA CTG				1778
Thr Val Phe	Ala Phe Ser Pro Glu Asn	Val Ser Lys Arg	Glu Arg Leu	
	415	420	425	
GTG TTT GAG CTG GGT CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTT				1826
Val Phe	Glu Leu Gly Leu Gly Ser Phe	Gln Gly Phe	Val Val Ala Val	
	430	435	440	
CTC TAT TGC TTT CTG AAT GGA GAG GTG CAG GCG GAG ATC AAG AGG AAG				1874
Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys				
	445	450	455	
TGG CGG AGC TGG AAG GTG AAC CGC TAC TTC ACC ATG GAC TTC AAG CAC				1922
Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe Lys His				
	460	465	470	475
CGG CAC CCA TCC CTG GCC AGC AGC GGG GTG AAC GGG GGC ACC CAG CTC				1970
Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu				
	480	485	490	
TCC ATC CTG AGC AAG AGC AGC TCC CAG ATC CGC ATG TCT GGG CTT CCG				2018
Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro				
	495	500	505	
GCC GAC AAC CTG GCC ACC TGAGCCCACC CTGCCCCCTC CTCTCCTCTG TACGCAGGC				2075
Ala Asp Asn Leu Ala Thr				
	510			
TGGGGCTGTG GTGGGGCGCC GGCCACGCA TGTTGTGCCT CTTCTCGCCT TCGGGCAGGC				2135
CCCGGGCTGG GCGCCTGGCC CCCGAGGTTG GAGAAGGATG CGGGACAGGC AGCTGTTTAG				2195
CCTTCCTGTT TTGGCGCTGG CCCAACCACC GTGGGTCCCT GGGCCTGCAC CCAGACATGT				2255
AATACTCCTT AATTGGGAAG TCATCCATTC TTTCCCTTTC CCAAGTCCTT GCTTATTAAG				2315
AGGTTCAAGT CACCTACCCA ATTCAGAAGC TTAAGTAACC ACTAACCACC GTGACTGCGT				2375
GGGAGGCCTC CCATGGGCTG AGCTACTGAC TTGGCTTTGG GGGCCTTGGG CTGGGGCCCT				2435
CCTTAAAGCC CCCCCTGAAA TTGTCGGACC TCAAAGTGTG ACTCCTTTGA GTCTACTCGC				2495
CACCCCGTG GCCCTTTGCA GCCCTGGTCC AGTCACCGAG GTTACTGGAA GTCCAGCTTG				2555
GATGGCCAGA CAGCTTTTGG GCACAGGCAG ACCCATGCTC ACCCAACATT TTAGTGTCCA				2615
GGTGCCAGG TGCCAGGTG CCCAGCTCCT GGGCATCAGA CAGTGGGAAA GCTCCAGGGA				2675
TCTACCATTC AGAGACTTCA GTTTGGATGT AGGGCTAAGG CCAGAGAAAA GTTCTGGAGC				2735
TTTTCATTTG GCCCAAGAAA AAAGTGCCAA GATCCAGAAA AGTGGATCTG AGTGGAAATT				2795
AGATGCAAAG AGCTTGGAG				2814

FIG. 2C

TGGCCTGCAC	CCCACCCCCC	AGCCTGCGAA	GACGGGGGGA	GGCGGTGGTC	GGTCGCCTCC	60		
CTCCTGCCCC	CGGCCTGGCT	TCGCGGTGGA	GGCGGTGCCT	CTCCGGCAAG	GCAGACCAGG	120		
CTGGGCGGAC	GCGCGGCGCG	GGGCGGGCTA	GGGAAGGCCG	GGGGCCTCGC	GCTCGGGCCC	180		
CGGGCGGCGA	CTGACAGCGG	CGGCGGCGGC	GGCAGCGGCT	CCAAGGCGAG	CGTGGTCCCC	240		
GCGTGCGCAC	AAGCTCGCCG	CCGCGCAGGG	ACCCACGGAC	ACCGGCGCCG	GGCGGACACA	300		
CAGACGCGGA	GATCGGGCTC	TACGCGCGCT	ACTCAGCGCA	CGAGCTCCCC	ATCCCTGGGC	360		
GGAGCGGGGC	GCGGACTCGC	CGCTGCGCGC	CCTCCCCGCG	GAGTCTGCC	CGGGCAGACC	420		
CGCAGCCCCG	GGCCCCGCCG	CGAGGCCCT	GGGTGAGCAG	CCTGTAGACA	CCTGGGGTTG	480		
AGCAGTGGCG	GCTGTGA	ATG AGA	GGC GGG	CGG CAC	TGG CCC	GAG CCG CCT	530	
		Met Arg	Gly Gly	Arg His	Trp Pro	Glu Pro Pro		
		1		5		10		
TGC AGG	CTG AGA	AGC GTC	ATG GCC	AGC ATC	GCG CAG	GTC TCC	CTG GCT	578
Cys Arg	Leu Arg	Ser Val	Met Ala	Ser Ile	Ala Gln	Val Ser	Leu Ala	
	15		20			25		
GCT CTC	CTC CTG	CTG CCT	ATG GCC	ACC GCC	ATG CAT	TCC GAC	TGC ATC	626
Ala Leu	Leu Leu	Leu Pro	Met Ala	Thr Ala	Met His	Ser Asp	Cys Ile	
	30		35	▲		40		
TTC AAG	AAG GAG	CAA GCC	ATG TGC	CTG GAG	AAG ATC	CAG AGG	GTG AAT	674
Phe Lys	Lys Glu	Gln Ala	Met Cys	Leu Glu	Lys Ile	Gln Arg	Val Asn	
	45		50		55			
GAC CTG	ATG GGC	TTG AAT	GAC TCC	TCC CCA	GGG TGC	CCT GGG	ATG TGG	722
Asp Leu	Met Gly	Leu Asn	Asp Ser	Ser Pro	Gly Cys	Pro Gly	Met Trp	
60		65		70			75	
GAC AAC	ATC ACG	TGT TGG	AAG CCC	GCC CAC	GTG GGT	GAG ATG	GTC CTG	770
Asp Asn	Ile Thr	Cys Trp	Lys Pro	Ala His	Val Gly	Glu Met	Val Leu	
	80			85		90		
GTC AGT	TGC CCT	GAA CTC	TTC CGA	ATC TTC	AAC CCA	GAC CAA	GTC TGG	818
Val Ser	Cys Pro	Glu Leu	Phe Arg	Ile Phe	Asn Pro	Asp Gln	Val Trp	
	95		100			105		
GAG ACG	GAA ACC	ATC GGA	GAG TTC	GGT TTT	GCA GAC	AGT AAA	TCC TTG	866
Glu Thr	Glu Thr	Ile Gly	Glu Phe	Gly Phe	Ala Asp	Ser Lys	Ser Leu	
	110		115		120			
GAT CTC	TCA GAC	ATG AGG	GTG GTG	AGC CGG	AAT TGC	ACG GAG	GAT GGA	914
Asp Leu	Ser Asp	Met Arg	Val Val	Ser Arg	Asn Cys	Thr Glu	Asp Gly	
	125		130		135			
TGG TCA	GAG CCA	TTC CCT	CAT TAT	TTC GAT	GCC TGT	GGG TTT	GAG GAG	962
Trp Ser	Glu Pro	Phe Pro	His Tyr	Phe Asp	Ala Cys	Gly Phe	Glu Glu	
140		145		150		155		
TAC GAA	TCT GAG	ACT GGG	GAC CAG	GAT TAC	TAC TAC	CTG TCA	GTG AAG	1010

FIG. 3A

Tyr	Glu	Ser	Glu	Thr	Gly	Asp	Gln	Asp	Tyr	Tyr	Tyr	Leu	Ser	Val	Lys	
				160					165					170		
GCC	CTG	TAC	ACA	GTT	GGC	TAC	AGC	ACG	TCC	CTC	GTC	ACC	CTC	ACC	ACT	1058
Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	Leu	Val	Thr	Leu	Thr	Thr	
			175					180					185			
GCC	ATG	GTC	ATC	CTG	TGT	CGT	TTC	CGG	AAG	CTG	CAC	TGC	ACC	CGC	AAC	1106
Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	Leu	His	Cys	Thr	Arg	Asn	
		190					195					200				
TTC	ATC	CAC	ATG	AAC	CTC	TTC	GTG	TCG	TTT	ATG	CTG	AGG	GCC	ATC	TCC	1154
Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	Ala	Ile	Ser	
	205					210					215					
GTC	TTC	ATC	AAA	GAC	TGG	ATC	CTC	TAT	GCT	GAG	CAG	GAC	AGC	AAT	CAC	1202
Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	Glu	Gln	Asp	Ser	Asn	His	
	220				225					230					235	
TGC	TTT	GTC	TCC	ACT	GTG	GAA	TGC	AAG	GCT	GTG	ATG	GTT	TTC	TTC	CAC	1250
Cys	Phe	Val	Ser	Thr	Val	Glu	Cys	Lys	Ala	Val	Met	Val	Phe	Phe	His	
				240					245					250		
TAC	TGT	GTT	GTA	TCC	AAC	TAC	TTC	TGG	CTG	TTC	ATC	GAG	GGC	CTG	TAT	1298
Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu	Phe	Ile	Glu	Gly	Leu	Tyr	
			255					260					265			
CTC	TTC	ACC	CTG	CTG	GTG	GAG	ACC	TTC	TTC	CCC	GAG	AGG	AGA	TAT	TTC	1346
Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe	Pro	Glu	Arg	Arg	Tyr	Phe	
		270					275					280				
TAC	TGG	TAC	ATC	ATC	ATT	GGC	TGG	GGG	ACA	CCA	ACT	GTG	TGT	GTG	TCT	1394
Tyr	Trp	Tyr	Ile	Ile	Ile	Gly	Trp	Gly	Thr	Pro	Thr	Val	Cys	Val	Ser	
	285					290					295					
GTG	TGG	GCT	ATG	CTG	AGG	CTC	TAC	TTC	GAT	GAC	ACA	GGC	TGC	TGG	GAT	1442
Val	Trp	Ala	Met	Leu	Arg	Leu	Tyr	Phe	Asp	Asp	Thr	Gly	Cys	Trp	Asp	
	300				305					310					315	
ATG	AAT	GAC	AAC	ACG	GCT	CTG	TGG	TGG	GTG	ATC	AAA	GGC	CCT	GTA	GTT	1490
Met	Asn	Asp	Asn	Thr	Ala	Leu	Trp	Trp	Val	Ile	Lys	Gly	Pro	Val	Val	
				320					325					330		
GGC	TCC	ATA	ATG	GTT	AAT	TTT	GTG	CTC	TTC	ATC	GGC	ATC	ATT	GTC	ATC	1538
Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe	Ile	Gly	Ile	Ile	Val	Ile	
			335					340					345			
CTT	GTG	CAG	AAA	CTT	CAG	TCT	CCA	GAC	ATG	GGA	GGC	AAC	GAG	TCC	AGC	1586
Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met	Gly	Gly	Asn	Glu	Ser	Ser	
		350					355					360				
ATC	TAC	TTA	CGG	CTC	GCC	AGG	TCC	ACC	TTG	CTG	CTC	ATC	CCA	CTC	TTT	1634
Ile	Tyr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro	Leu	Phe	
	365					370					375					

FIG. 3B

GGA ATC CAC TAC ACT GTC TTT GCT TTC TCC CCG GAG AAC GTC AGC AAG Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys 380 385 390 395	1682
AGG GAG AGA CTG GTG TTT GAG CTG GGT CTG GGC TCC TTC CAG GGC TTT Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe 400 405 410	1730
GTG GTG GCT GTT CTC TAT TGC TTT CTG AAT GGA GAG GTG CAG GCG GAG Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu 415 420 425	1778
ATC AAG AGG AAG TGG CGG AGC TGG AAG GTG AAC CGC TAC TTC ACC ATG Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met 430 435 440	1826
GAC TTC AAG CAC CGG CAC CCA TCC CTG GCC AGC AGC GGG GTG AAC GGG Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly 445 450 455	1874
GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAG ATC CGC ATG Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met 460 465 470 475	1922
TCT GGG CTT CCG GCC GAC AAC CTG GCC ACC TGAGCCCACC CTGCCCCCTC CTCT Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr 480 485	1976
CCTCTGTACG CAGGCTGGGG CTGTGGTGGG GCGCCGGCCC ACGCATGTTG TGCCTCTTCT CGCCTTCGGG CAGGCCCCGG GCTGGGCGCC TGGCCCCCGA GGTTGGAGAA GGATGCGGGA CAGGCAGCTG TTTAGCCTTC CTGTTTTGGC GCTGGCCCAA CCACCGTGGG TCCCTGGGCC TGCACCCAGA CATGTAATAC TCCTTAATTG GGAAGTCATC CATTCTTTCC CTTTCCCAAG TCCTTGCTTA TTAAGAGGTT CAAGTCACCT ACCCAATTCA GAAGCTTAAG TAACCACTAA CCACCGTGAC TGC GTGGGAG GCCTCCCATG GGCTGAGCTA CTGACTTGGC TTTGGGGGCC TTGGGCTGGG GCCCTCCTTA AAGCCCCCCC TGAAATTGTC GGACCTCAA GTGTGACTCC TTTGAGTCTA CTCGCCACCC CCGTGGCCCT TTGCAGCCCT GGTCCAGTCA CCGAGGTTAC TGGAAGTCCA GCTTGGATGG CCAGACAGCT TTTTGGCACA GGCAGACCCA TGCTCACCCA ACATTTTAGT GTCCAGGTGC CCAGGTGCCC AGGTGCCAG CTCCTGGGCA TCAGACAGTG GGAAAGCTCC AGGGATCTAC CATTGAGAGA CTTGAGTTTG GATGTAGGGC TAAGGCCAGA GAAAAGTTCT GGAGCTTTTC ATTTGGCCCA AGAAAAAACT GCCAAGATCC AGAAAAGTGG ATCTGAGTGG AATTTAGATG CAAAGAGCTT GGAG	2036 2096 2156 2216 2276 2336 2396 2456 2516 2576 2636 2696 2730

FIG. 3C

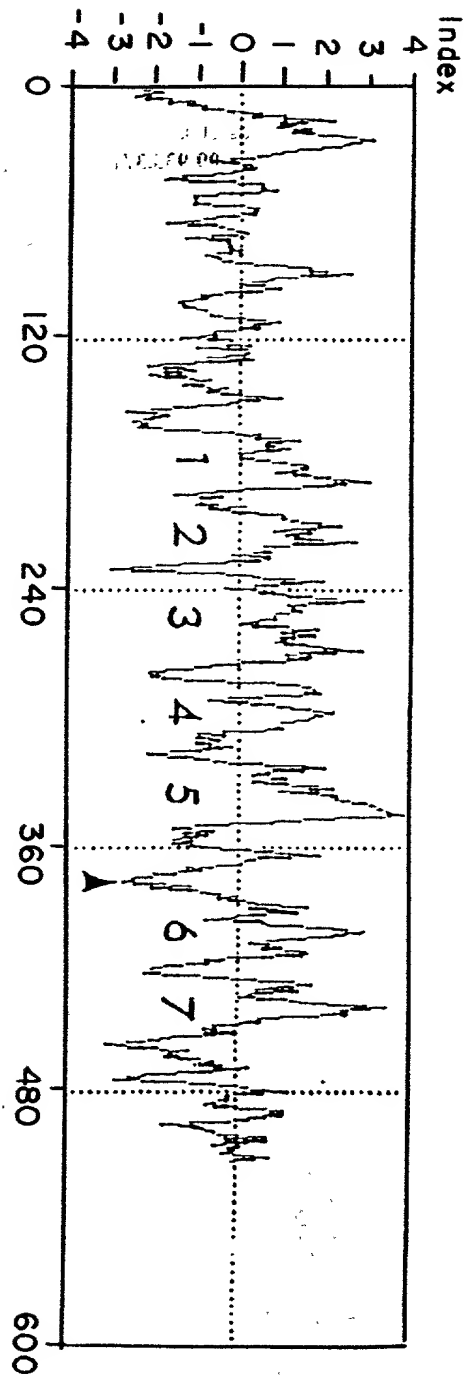


FIG. 5A

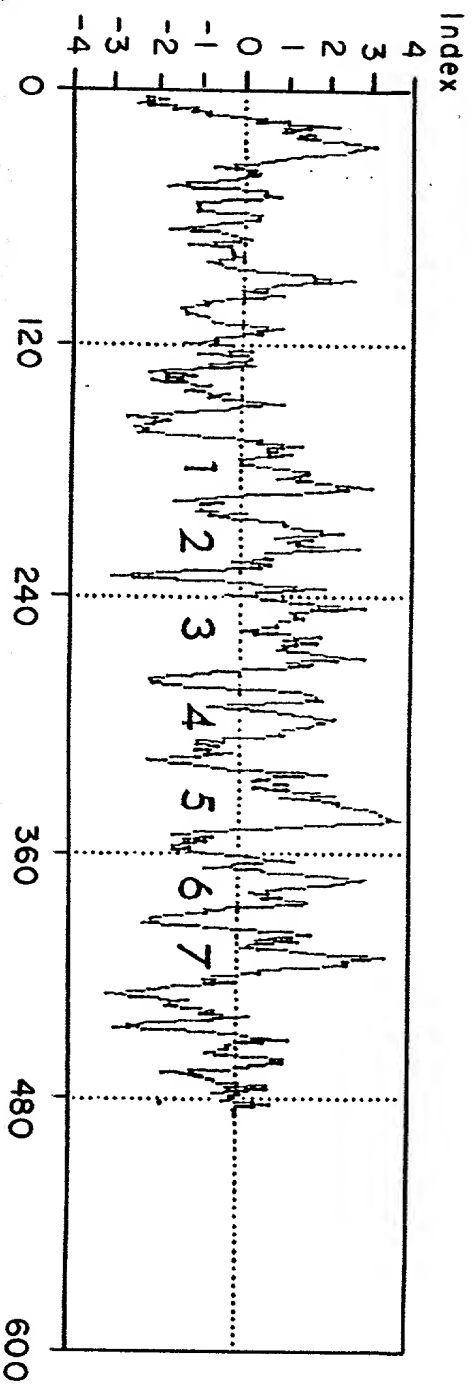


FIG. 5B

CGAGTGGACA GTGGCAGGCG GTGACTGAAT CTCCAAGTCT GGAAACAATA GCCAGAGATA	60
GTGGCTGGGA AGCACC ATG GCC AGA GTC CTG CAG CTC TCC CTG ACT GCT CTC	112
Met Ala Arg Val Leu Gln Leu Ser Leu Thr Ala Leu	
1 5 10	
CTG CTG CCT GTG GCT ATT GCT ATG CAC TCT GAC TGC ATC TTC AAG AAG	160
Leu Leu Pro Val Ala Ile Ala Met His Ser Asp Cys Ile Phe Lys Lys	
15 20 25	
GAG CAA GCC ATG TGC CTG GAG AGG ATC CAG AGG GCC AAC GAC CTG ATG	208
Glu Gln Ala Met Cys Leu Glu Arg Ile Gln Arg Ala Asn Asp Leu Met	
30 35 40	
GGA CTA AAC GAG TCT TCC CCA GGT TGC CCT GGC ATG TGG GAC AAT ATC	256
Gly Leu Asn Glu Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile	
45 50 55 60	
ACA TGT TGG AAG CCA GCT CAA GTA GGT GAG ATG GTC CTT GTA AGC TGC	304
Thr Cys Trp Lys Pro Ala Gln Val Gly Glu Met Val Leu Val Ser Cys	
65 70 75	
CCT GAG GTC TTC CGG ATC TTC AAC CCG GAC CAA GTC TGG ATG ACA GAA	352
Pro Glu Val Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Met Thr Glu	
80 85 90	
ACC ATA GGA GAT TCT GGT TTT GCC GAT AGT AAT TCC TTG GAG ATC ACA	400
Thr Ile Gly Asp Ser Gly Phe Ala Asp Ser Asn Ser Leu Glu Ile Thr	
95 100 105	
GAC ATG GGG GTC GTG GGC CGG AAC TGC ACA GAG GAC GGC TGG TCG GAG	448
Asp Met Gly Val Val Gly Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu	
110 115 120	
CCC TTC CCC CAC TAC TTC GAT GCT TGT GGG TTT GAT GAT TAT GAG CCT	496
Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Asp Tyr Glu Pro	
125 130 135 140	
GAG TCT GGA GAT CAG GAT TAT TAC TAC CTG TCG GTG AAG GCT CTC TAC	544
Glu Ser Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr	
145 150 155	
ACA GTC GGC TAC AGC ACT TCC CTC GCC ACC CTC ACT ACT GCC ATG GTC	592
Thr Val Gly Tyr Ser Thr Ser Leu Ala Thr Leu Thr Thr Ala Met Val	
160 165 170	
ATC TTG TGC CGC TTC CGG AAG CTG CAT TGC ACT CGC AAC TTC ATC CAC	640
Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His	
175 180 185	
ATG AAC CTG TTT GTA TCC TTC ATG CTG AGG GCT ATC TCC GTC TTC ATC	688
Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile	

FIG. 7A

190	195	200	
AAG Lys 205	GAC Asp 210	TGG Trp 215	736
TCC Ser	ACC Thr	GTG Val	784
GTG Val	TCC Ser	AAC Asn	832
CTG Leu	CTG Leu	GTG Val	880
ACC Thr	ATC Ile	ATC Ile	928
GTG Val	CTG Leu	AGG Arg	976
AGC Ser	ACA Thr	GCT Ala	1024
ATG Met	GTT Val	AAC Asn	1072
AAG Lys	CTG Leu	CAG Gln	1120
CGG Arg	CTG Leu	GCC Ala	1168
TAC Tyr	ACA Thr	GTA Val	1216
CTT Leu	GTG Val	TTT Phe	1264
GTA Val	CTC Leu	TAC Tyr	1312

FIG. 7B

AAA	TGG	AGG	AGC	TGG	AAG	GTG	AAC	CGT	TAC	TTC	ACT	ATG	GAC	TTC	AAG	1360
Lys	Trp	Arg	Ser	Trp	Lys	Val	Asn	Arg	Tyr	Phe	Thr	Met	Asp	Phe	Lys	
	415						420					425				
CAC	CGG	CAC	CCG	TCC	CTG	GCC	AGC	AGT	GGA	GTA	AAT	GGG	GGA	ACC	CAG	1408
His	Arg	His	Pro	Ser	Leu	Ala	Ser	Ser	Gly	Val	Asn	Gly	Gly	Thr	Gln	
	430					435					440					
CTG	TCC	ATC	CTG	AGC	AAG	AGC	AGC	TCC	CAG	CTC	CGC	ATG	TCC	AGC	CTC	1456
Leu	Ser	Ile	Leu	Ser	Lys	Ser	Ser	Ser	Gln	Leu	Arg	Met	Ser	Ser	Leu	
445					450					455					460	
CCG	GCC	GAC	AAC	TTG	GCC	ACC	TGAGGCCTGT	CTCCCTCCTC	CTTCTGCACA	GGCTG	1512					
Pro	Ala	Asp	Asn	Leu	Ala	Thr	***									
				465												
GGGCTGCGGG	CCAGTGCCTG	AGCATGTTTG	TGCCTCTCCC	CTCTCCTTGG	GCAGGCCCTG	1572										
GGTAGGAAGC	TGGGCTCCTC	CCCAAAGGGG	AAGAGAGAGA	TAGGGTATAG	GCTGATATTG	1632										
CTCCTCCTGT	TTGGGTCCCA	CCTACTGTGA	TTCATTGAGC	CTGATTTGAC	ATGTAAATAC	1692										
ACCTCAAATT	TGGAAAGTTG	CCCCATCTCT	GCCCCCAACC	CATGCCCTG	CTCACCTCTG	1752										
CCAGGCCCCA	GCTCAACCTA	CTGTGTCAAG	GCCAGCCTCA	GTGATAGTCT	GATCCCAGGT	1812										
ACAAGGCCTT	GTGAGCTGAG	GCTGAAAGGC	CTGTTTTGGA	GAGGCTGGGG	TAGTGCC	1869										

FIG. 8

CGAGTGGACA GTGGCAGGCG GTGACTGAAT CTCCAAGTCT GGAAACAATA GCCAGAGATA	60
GTGGCTGGGA AGCACC ATG GCC AGA GTC CTG CAG CTC TCC CTG ACT GCT CTC	112
Met Ala Arg Val Leu Gln Leu Ser Leu Thr Ala Leu	
1 5 10	
CTG CTG CCT GTG GCT ATT GCT ATG CAC TCT GAC TGC ATC TTC AAG AAG	160
Leu Leu Pro Val Ala Ile Ala Met His Ser Asp Cys Ile Phe Lys Lys	
15 20 25	
GAG CAA GCC ATG TGC CTG GAG AGG ATC CAG AGG GCC AAC GAC CTG ATG	208
Glu Gln Ala Met Cys Leu Glu Arg Ile Gln Arg Ala Asn Asp Leu Met	
30 35 40	
GGA CTA AAC GAG TCT TCC CCA GGT TGC CCT GGC ATG TGG GAC AAT ATC	256
Gly Leu Asn Glu Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile	
45 50 55 60	
ACA TGT TGG AAG CCA GCT CAA GTA GGT GAG ATG GTC CTT GTA AGC TGC	304
Thr Cys Trp Lys Pro Ala Gln Val Gly Glu Met Val Leu Val Ser Cys	
65 70 75	
CCT GAG GTC TTC CGG ATC TTC AAC CCG GAC CAA GTC TGG ATG ACA GAA	352
Pro Glu Val Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Met Thr Glu	
80 85 90	
ACC ATA GGA GAT TCT GGT TTT GCC GAT AGT AAT TCC TTG GAG ATC ACA	400
Thr Ile Gly Asp Ser Gly Phe Ala Asp Ser Asn Ser Leu Glu Ile Thr	
95 100 105	
GAC ATG GGG GTC GTG GGC CGG AAC TGC ACA GAG GAC GGC TGG TCG GAG	448
Asp Met Gly Val Val Gly Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu	
110 115 120	
CCC TTC CCC CAC TAC TTC GAT GCT TGT GGG TTT GAT GAT TAT GAG CCT	496
Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Asp Tyr Glu Pro	
125 130 135 140	
GAG TCT GGA GAT CAG GAT TAT TAC TAC CTG TCG GTG AAG GCT CTC TAC	544
Glu Ser Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr	
145 150 155	
ACA GTC GGC TAC AGC ACT TCC CTC GCC ACC CTC ACT ACT GCC ATG GTC	592
Thr Val Gly Tyr Ser Thr Ser Leu Ala Thr Leu Thr Thr Ala Met Val	
160 165 170	
ATC TTG TGC CGC TTC CGG AAG CTG CAT TGC ACT CGC AAC TTC ATC CAC	640
Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His	
175 180 185	
ATG AAC CTG TTT GTA TCC TTC ATG CTG AGG GCT ATC TCC GTC TTC ATC	688
Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile	
190 195 200	

FIG. 9A

AAG Lys 205	GAC Asp	TGG Trp	ATC Ile	TTG Leu	TAC Tyr 210	GCC Ala	GAG Glu	CAG Gln	GAC Asp 215	AGC Ser	AGT Ser	CAC His	TGC Cys	TTC Phe	GTT Val 220	736
TCC Ser	ACC Thr	GTG Val	GAG Glu	TGC Cys 225	AAA Lys	GCT Ala	GTC Val	ATG Met	GTT Val 230	TTC Phe	TTC Phe	CAC His	TAC Tyr	TGC Cys 235	GTG Val	784
GTG Val	TCC Ser	AAC Asn	TAC Tyr 240	TTT Phe	TGG Trp	CTG Leu	TTC Phe	ATT Ile 245	GAA Glu	GGC Gly	CTG Leu	TAC Tyr	CTC Leu 250	TTT Phe	ACA Thr	832
CTG Leu	CTG Leu	GTG Val 255	GAG Glu	ACC Thr	TTC Phe	TTC Phe	CCT Pro 260	GAG Glu	AGG Arg	AGA Arg	TAT Tyr	TTC Phe 265	TAC Tyr	TGG Trp	TAC Tyr	880
ACC Thr	ATC Ile 270	ATC Ile	GGC Gly	TGG Trp	GGG Gly	ACA Thr 275	CCT Pro	ACT Thr	GTG Val	TGT Cys	GTA Val 280	ACA Thr	GTG Val	TGG Trp	GCT Ala	928
GTG Val 285	CTG Leu	AGG Arg	CTC Leu	TAT Tyr	TTT Phe 290	GAT Asp	GAT Asp	GCA Ala	GGA Gly	TGC Cys 295	TGG Trp	GAT Asp	ATG Met	AAT Asn	GAC Asp 300	976
AGC Ser	ACA Thr	GCT Ala	CTG Leu	TGG Trp 305	TGG Trp	GTG Val	ATC Ile	AAA Lys	GGC Gly 310	CCC Pro	GTG Val	GTT Val	GGC Gly	TCT Ser 315	ATA Ile	1024
ATG Met	GTT Val	AAC Asn	TTT Phe 320	GTG Val	CTT Leu	TTC Phe	ATC Ile	GGC Gly 325	ATC Ile	ATC Ile	ATC Ile	ATC Ile	CTT Leu 330	GTA Val	CAG Gln	1072
AAG Lys	CTG Leu	CAG Gln 335	TCC Ser	CCA Pro	GAC Asp	ATG Met	GGA Gly 340	GGC Gly	AAC Asn	GAG Glu	TCC Ser	AGC Ser 345	ATC Ile	TAC Tyr	TTT Phe △	1120
AGC Ser 350	TGC Cys	GTG Val	CAG Gln	AAA Lys	TGC Cys	TAC Tyr 355	TGC Cys	AAG Lys	CCA Pro	CAG Gln	CGG Arg 360	GCT Ala	CAG Gln	CAG Gln	CAC His	1168
TCT Ser 365	TGC Cys	AAG Lys	ATG Met	TCA Ser	GAA Glu	CTA Leu 370	TCC Ser	ACC Thr	ATT Ile	ACT Thr 375	CTA Leu △	CGG Arg	CTG Leu	GCC Ala	CGC Arg 380	1216
TCC Ser	ACC Thr	CTA Leu	CTG Leu	CTC Leu	ATC Ile	CCA Pro	CTC Leu	TTC Phe	GGA Gly 390	ATC Ile	CAC His	TAC Tyr	ACA Thr	GTA Val 395	TTT Phe	1264
GCC Ala	TTC Phe	TCT Ser	CCA Pro 400	GAG Glu	AAC Asn	GTC Val	AGC Ser	AAG Lys 405	AGG Arg	GAA Glu	AGA Arg	CTT Leu	GTG Val 410	TTT Phe	GAG Glu	1312
CTT Leu	GGG Gly	CTG Leu	GGC Gly	TCC Ser	TTC Phe	CAG Gln	GGC Gly	TTT Phe	GTG Val	GTG Val	GCT Ala	GTA Val	CTC Leu	TAC Tyr	TGC Cys	1360

FIG. 9B

415	420	425	
TTC CTG AAT GGG GAG GTA CAG GCA GAG ATT AAG AGG AAA TGG AGG AGC			1408
Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser			
430	435	440	
TGG AAG GTG AAC CGT TAC TTC ACT ATG GAC TTC AAG CAC CGG CAC CCG			1456
Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe Lys His Arg His Pro			
445	450	455	460
TCC CTG GCC AGC AGT GGA GTA AAT GGG GGA ACC CAG CTG TCC ATC CTG			1504
Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu			
	465	470	475
AGC AAG AGC AGC TCC CAG CTC CGC ATG TCC AGC CTC CCG GCC GAC AAC			1552
Ser Lys Ser Ser Ser Gln Leu Arg Met Ser Ser Leu Pro Ala Asp Asn			
	480	485	490
TTG GCC ACC TGAGGCCTGT CTCCCTCCTC CTTCTGCACA GGCTGGGGCT GCGGGCCAGT			1611
Leu Ala Thr ***			
495			
GCCTGAGCAT GTTTGTGCCT CTCCCCTCTC CTTGGGCAGG CCCTGGGTAG GAAGCTGGGC			1671
TCCTCCCCAA AGGGGAAGAG AGAGATAGGG TATAGGCTGA TATTGCTCCT CCTGTTTGGG			1731
TCCCACCTAC TGTGATTCAT TGAGCCTGAT TTGACATGTA AATACACCTC AAATTTGGAA			1791
AGTTGCCCCA TCTCTGCCCC CAACCCATGC CCCTGCTCAC CTCTGCCAGG CCCCAGCTCA			1851
ACCTACTGTG TCAAGGCCAG CCTCAGTGAT AGTCTGATCC CAGGTACAAG GCCTTGTGAG			1911
CTGAGGCTGA AAGGCCTGTT TTGGAGAGGC TGGGGTAGTG CCCACCCAG CAGCCTTTCA			1971
GCAAATTGAC TTTGGATGTG GACCCCTTCT AGCCTGTACC AAGTACTGCA GTTGGCTAGG			2031
GATGCAGCTC AGTTTCCTGA GCATCCTTTG GAGCAGGTCA ACCTGAGGCT CCTTTTGCTT			2091
ACCCGACATC TAAGTTGTCC AGGTGCTCGG CTCCTGTGTG CCTGGATGAC GGGAGGGCTC			2151
CGGGGTCTTT CAGTCAAAGA CTTACATTGA GGTGGGGTGA GAGTCAGAGA AAAGTTCTGG			2211
TGCTTTTCAT TTGTTCTAAG AGCTGAGAGC CAGGAATGCA GAGTCAATTG GGAAGGAGAT			2271
GGGATAGCTG ATGATCTTAC CATGTCCATG ACTGTGCCCC TGATTCAAGA CCGGATCATG			2331
TGGTGGCTTT ATTTCTACAC TTCTTGTTCA CAATGGACAG TCTGAGGAAG CTCTTCTTTC			2391
AGCCACAACA ACCACAGAAA GCCCTTTCTT CTCCCCTCTT GTTCTCCAT AAGTCAAAGC			2451
CATGTTTAGA ACGGACCAGC CACCTTGCGA TGAATCACT GAGTTCTGAA GCAACTTTCA			2511
ATTTCCACGA GCCAAGTCCT GGGTCCAGGG ACGCCCC			2548

FIG. 10

Rat	Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu
	* * * * *
Bovine	Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu
	1 5 10 15
Rat	Arg Ile Gln Arg Ala Asn Asp Leu Met Gly Leu Asn Glu
	* * * * *
Bovine	Lys Ile Gln Arg Val Asn Asp Leu Met Gly Leu Asn Asp
	20 25

FIG. 11

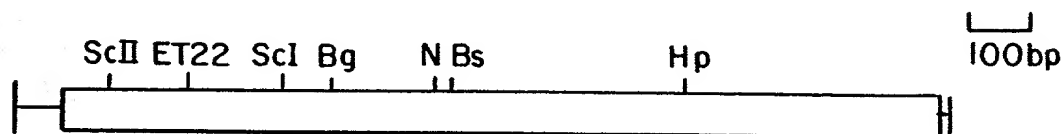


FIG. 12

Human	Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu
	* * * * *
Bovine	Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu
Human	Gly Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp
	* * * * *
Bovine	Glu Lys Ile Gln Arg Val Asn Asp Leu Met Gly Leu Asn Asp

FIG. 14

AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG	60
GCCAAGAAGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC	109
Met Ala Gly Val Val His Val Ser Leu Ala Ala His	
1 5 10	
TGC GGG GCC TGT CCG TGG GGC CGG GGC AGA CTC CGC AAA GGA CGC GCA	157
Cys Gly Ala Cys Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala	
15 20 25	
GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG	205
Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu	
30 35 40	
CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT	253
Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly	
45 50 55 60	
GTC GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT	301
Val Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro	
65 70 75	
GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG	349
Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu	
80 85 90	
GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT	397
Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser	
95 100 105	
CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC	445
Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala	
110 115 120	
CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC	493
His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile	
125 130 135 140	
TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT	541
Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp	
145 150 155	
TTT GGT GAC AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC	589
Phe Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser	
160 165 170	
CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA CCC TTC CCT CAT TAC TTT	637
Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe	
175 180 185	
GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT	685
Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp	

FIG. 13A

190					195					200						
TAT Tyr 205	TAC Tyr	TAC Tyr	CTG Leu	TCA Ser	GTG Val 210	AAG Lys	GCC Ala	CTC Leu	TAC Tyr	ACG Thr 215	GTT Val	GGC Gly	TAC Tyr	AGC Ser	ACA Thr 220	733
TCC Ser	CTC Leu	GTC Val	ACC Thr 225	CTC Leu	ACC Thr	ACT Thr	GCC Ala	ATG Met	GTC Val 230	ATC Ile	CTT Leu	TGT Cys	CGC Arg	TTC Phe 235	CGG Arg	781
AAG Lys	CTG Leu	CAC His	TGC Cys 240	ACA Thr	CGC Arg	AAC Asn	TTC Phe	ATC Ile 245	CAC His	ATG Met	AAC Asn	CTG Leu	TTT Phe 250	GTG Val	TCG Ser	829
TTC Phe	ATG Met	CTG Leu 255	AGG Arg	GCG Ala	ATC Ile	TCC Ser	GTC Val 260	TTC Phe	ATC Ile	AAA Lys	GAC Asp	TGG Trp 265	ATT Ile	CTG Leu	TAT Tyr	877
GCG Ala	GAG Glu 270	CAG Gln	GAC Asp	AGC Ser	AAC Asn	CAC His 275	TGC Cys	TTC Phe	ATC Ile	TCC Ser	ACT Thr 280	GTG Val	GAA Glu	TGT Cys	AAG Lys	925
GCC Ala 285	GTC Val	ATG Met	GTT Val	TTC Phe	TTC Phe 290	CAC His	TAC Tyr	TGT Cys	GTT Val	GTG Val 295	TCC Ser	AAC Asn	TAC Tyr	TTC Phe	TGG Trp 300	973
CTG Leu	TTC Phe	ATC Ile	GAG Glu	GGC Gly 305	CTG Leu	TAC Tyr	CTC Leu	TTC Phe	ACT Thr 310	CTG Leu	CTG Leu	GTG Val	GAG Glu	ACC Thr 315	TTC Phe	1021
TTC Phe	CCT Pro	GAA Glu	AGG Arg 320	AGA Arg	TAC Tyr	TTC Phe	TAC Tyr	TGG Trp 325	TAC Tyr	ACC Thr	ATC Ile	ATT Ile	GGC Gly 330	TGG Trp	GGG Gly	1069
TCC Ser	CCA Pro	ACT Thr 335	GTG Val	TGT Cys	GTG Val	ACA Thr	GTG Val 340	TGG Trp	GCT Ala	ACG Thr	CTG Leu	AGA Arg 345	CTC Leu	TAC Tyr	TTT Phe	1117
GAT Asp	GAC Asp 350	ACA Thr	GGC Gly	TGC Cys	TGG Trp	GAT Asp 355	ATG Met	AAT Asn	GAC Asp	AGC Ser	ACA Thr 360	GCT Ala	CTG Leu	TGG Trp	TGG Trp	1165
GTG Val 365	ATC Ile	AAA Lys	GGC Gly	CCT Pro	GTG Val 370	GTT Val	GGC Gly	TCT Ser	ATC Ile	ATG Met 375	GTT Val	AAC Asn	TTT Phe	GTG Val	CTT Leu 380	1213
TTT Phe	ATT Ile	GGC Gly	ATT Ile	ATC Ile 385	GTC Val	ATC Ile	CTT Leu	GTG Val 390	CAG Gln	AAA Lys	CTT Leu	CAG Gln	TCT Ser	CCA Pro 395	GAC Asp	1261
ATG Met	GGA Gly	GGC Gly	AAT Asn 400	GAG Glu	TCC Ser	AGC Ser	ATC Ile	TAC Tyr 405	TTG Leu	CGA Arg	CTG Leu	GCC Ala	CGG Arg 410	TCC Ser	ACC Thr	1309

FIG. 13B

CTG	CTG	CTC	ATC	CCA	CTA	TTC	GGA	ATC	CAC	TAC	ACA	GTA	TTT	GCC	TTC	1357
Leu	Leu	Leu	Ile	Pro	Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	
		415					420					425				
TCC	CCA	GAG	AAT	GTC	AGC	AAA	AGG	GAA	AGA	CTC	GTG	TTT	GAG	CTG	GGG	1405
Ser	Pro	Glu	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	
	430					435					440					
CTG	GGC	TCC	TTC	CAG	GGC	TTT	GTG	GTG	GCT	GTT	CTC	TAC	TGT	TTT	CTG	1453
Leu	Gly	Ser	Phe	Gln	Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	
445				450						455					460	
AAT	GGT	GAG	GTA	CAA	GCG	GAG	ATC	AAG	CGA	AAA	TGG	CGA	AGC	TGG	AAG	1501
Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	
				465					470					475		
GTG	AAC	CGT	TAC	TTC	GCT	GTG	GAC	TTC	AAG	CAC	CGA	CAC	CCG	TCT	CTG	1549
Val	Asn	Arg	Tyr	Phe	Ala	Val	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	
			480					485					490			
GCC	AGC	AGT	GGG	GTG	AAT	GGG	GGC	ACC	CAG	CTC	TCC	ATC	CTG	AGC	AAG	1597
Ala	Ser	Ser	Gly	Val	Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	
		495					500					505				
AGC	AGC	TCC	CAA	ATC	CGC	ATG	TCT	GGC	CTC	CCT	GCT	GAC	AAT	CTG	GCC	1645
Ser	Ser	Ser	Gln	Ile	Arg	Met	Ser	Gly	Leu	Pro	Ala	Asp	Asn	Leu	Ala	
	510					515					520					
ACC	TGAGCCATGC	TCCCCT														1664
Thr																
525																

FIG. 13C

Rat
Type I-B Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys
AAC GAG TCC AGC ATC TAC TTC ▲ AGC TGC GTG CAG AAA TGC TAC TGC AAA

pHRP15A
human Type I-B Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys
AAT GAG TCC AGC ATC TAC TTC ▲ AGC TGC GTG CAG AAA TGC TAC TGC AAG

pHRP55A
Type I-B2 Asn Glu Ser Ser Ile Tyr Phe — Cys Val Gln Lys Cys Tyr Cys Lys
AAT GAG TCC AGC ATC TAC TTC — TGC GTG CAG AAA TGC TAC TGC AAG

pHRP66P
Type I-C Asn Glu Ser Ser Ile Tyr Leu Thr Asn Leu Ser Pro Arg Val Pro Lys
AAT GAG TCC AGC ATC TAC TTA ACA AAT TTA AGC CCG CGA GTC CCC AAG

Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr
CCA CAG CGG CGT CAG CAG CAC TCT TGC AAG ATC TCA GAA CTA TCC ACC

Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr
CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC

Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr
CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC

Lys Ala Arg Glu Asp Pro Leu Pro Val Pro Ser Asp Gln His Ser Leu
AAA GCC CGA GAG GAC CCC CTG CCT GTG CCC TCA GAC CAG CAT TCA CTC

Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu
ATT ACT CTA CGG CTG GCC CGC TCC ACC CTA

Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu
ATT ACT CTG CGA CTG GCC CGG TCC ACC CTG

Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu
ATT ACT CTG CGA CTG GCC CGG TCC ACC CTG

Pro Phe Leu Arg Leu Ala Arg Ser Thr Leu
CCT TTC CTG CGA CTG GCC CGG TCC ACC CTG

FIG. 15

AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG	60
GCCAAGAAAGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC	109
Met Ala Gly Val Val His Val Ser Leu Ala Ala His	
1 5 10	
TGC GGG GCC TGT CCG TGG GGC CGG GGC AGA CTC CGC AAA GGA CGC GCA	157
Cys Gly Ala Cys Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala	
15 20 25	
GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG	205
Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu	
30 35 40	
CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT	253
Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly	
45 50 55 60	
GTC GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT	301
Val Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro	
65 70 75	
GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG	349
Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu	
80 85 90	
GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT	397
Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser	
95 100 105	
CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC	445
Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala	
110 115 120	
CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC	493
His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile	
125 130 135 140	
TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT	541
Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp	
145 150 155	
TTT GGT GAC AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC	589
Phe Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser	
160 165 170	
CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA CCC TTC CCT CAT TAC TTT	637
Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe	
175 180 185	
GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT	685
Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp	

FIG. 16A

190	195	200	
TAT Tyr 205	TAC Tyr	TAC Tyr	733
CTG Leu	TCA Ser	GTG Val 210	
AAG Lys	GCC Ala	CTC Leu	
TAC Tyr	ACG Thr 215	GTT Val	
GGC Gly	TAC Tyr	AGC Ser	
ACA Thr 220			
TCC Ser	CTC Leu	GTC Val 230	781
CTC Leu	GTC Val	ACC Thr 225	
CTC Leu	ACC Thr	ACT Thr	
GCC Ala	ATG Met	GTC Val	
ATC Ile	CTT Leu	TGT Cys	
CGC Arg	TTC Phe	CGG Arg 235	
AAG Lys	CTG Leu	CAC His	829
CTG Leu	CAC His	ATG Met	
CAC His	ATG Met	AAC Asn	
CTG Leu	TTT Phe	GTG Val	
TCG Ser			
TTC Phe	ATG Met	CTG Leu	877
ATG Met	CTG Leu	AGG Arg 255	
CTG Leu	AGG Arg	GCG Ala	
ATC Ile	TCC Ser	GTC Val 260	
AAA Lys	GAC Asp	TGG Trp 265	
GAG Glu 270	CAG Gln	GAC Asp	925
GAG Glu	AGC Ser	AAC Asn	
CAG Gln	AGC Ser	CAC His 275	
GAC Asp	AAC Asn	TGC Cys	
AGC Ser	CAC His	TTC Phe	
AAC Asn	TGC Cys	ATC Ile	
CAC His	TTC Phe	TCC Ser	
TGC Cys	ATC Ile	ACT Thr 280	
TTC Phe	ATC Ile	GTG Val	
ATC Ile	TCC Ser	GAA Glu	
GTG Val	AAC Asn	TGT Cys	
TCC Ser	AAC Asn	TAT Tyr	973
AAC Asn	TAT Tyr	TTC Phe	
TAT Tyr	TTC Phe	TGG Trp 300	
CTG Leu	TTC Phe	ATC Ile	1021
TTC Phe	ATC Ile	GAG Glu 305	
ATC Ile	GAG Glu	GGC Gly	
GAG Glu	GGC Gly	CTG Leu	
GGC Gly	CTG Leu	TAC Tyr	
CTG Leu	TAC Tyr	CTC Leu	
TAC Tyr	CTC Leu	TTC Phe	
CTC Leu	TTC Phe	ACT Thr 310	
TTC Phe	ACT Thr	CTG Leu	
ACT Thr	CTG Leu	GTG Val	
CTG Leu	GTG Val	GAG Glu 315	
GTG Val	GAG Glu	ACC Thr	
GAG Glu	ACC Thr	TTC Phe	
ACC Thr	TTC Phe	TGG Trp	1069
TTC Phe	TGG Trp	GGG Gly	
CCT Pro	GAA Glu	AGG Arg 320	
GAA Glu	AGG Arg	AGA Arg	
AGG Arg	AGA Arg	TAC Tyr	
AGA Arg	TAC Tyr	TTC Phe	
TAC Tyr	TTC Phe	TAC Tyr	
TTC Phe	TAC Tyr	TGG Trp 325	
TAC Tyr	TGG Trp	TAC Tyr	
TGG Trp	TAC Tyr	ACC Thr	
TAC Tyr	ACC Thr	ATC Ile	
ACC Thr	ATC Ile	ATT Ile	
ATC Ile	ATT Ile	GGC Gly 330	
ATT Ile	GGC Gly	TGG Trp	
GGC Gly	TGG Trp	GGG Gly	
TGG Trp	GGG Gly		
ACC Thr	CCA Pro	ACT Thr 335	1117
CCA Pro	ACT Thr	GTG Val	
ACT Thr	GTG Val	TGT Cys	
GTG Val	TGT Cys	GTG Val	
TGT Cys	GTG Val	ACA Thr	
GTG Val	ACA Thr	GTG Val 340	
ACA Thr	GTG Val	TGG Trp	
GTG Val	TGG Trp	GCT Ala	
TGG Trp	GCT Ala	ACG Thr	
GCT Ala	ACG Thr	CTG Leu	
ACG Thr	CTG Leu	AGA Arg 345	
CTG Leu	AGA Arg	CTC Leu	
AGA Arg	CTC Leu	TAC Tyr	
CTC Leu	TAC Tyr	TTT Phe	
TAC Tyr	TTT Phe		
TTT Phe			
GAT Asp 350	GAC Asp	ACA Thr 350	1165
GAC Asp	ACA Thr	GGC Gly	
ACA Thr	GGC Gly	TGC Cys	
GGC Gly	TGC Cys	TGG Trp	
TGC Cys	TGG Trp	GAT Asp 355	
TGG Trp	GAT Asp	ATG Met	
GAT Asp	ATG Met	AAT Asn	
ATG Met	AAT Asn	GAC Asp	
AAT Asn	GAC Asp	AGC Ser	
GAC Asp	AGC Ser	ACA Thr 360	
AGC Ser	ACA Thr	GCT Ala	
ACA Thr	GCT Ala	CTG Leu	
GCT Ala	CTG Leu	TGG Trp	
CTG Leu	TGG Trp	TGG Trp	
TGG Trp	TGG Trp		
GTG Val 365	ATC Ile	AAA Lys	1213
ATC Ile	AAA Lys	GGC Gly	
AAA Lys	GGC Gly	CCT Pro	
GGC Gly	CCT Pro	GTG Val 370	
CCT Pro	GTG Val	GTT Val	
GTG Val	GTT Val	GGC Gly	
GTT Val	GGC Gly	TCT Ser	
GGC Gly	TCT Ser	ATC Ile	
TCT Ser	ATC Ile	ATG Met 375	
ATC Ile	ATG Met	GTT Val	
ATG Met	GTT Val	AAC Asn	
GTT Val	AAC Asn	TTT Phe	
AAC Asn	TTT Phe	GTG Val 380	
TTT Phe	GTG Val	CTT Leu	
GTG Val	CTT Leu	CAG Gln 390	
CTT Leu	CAG Gln	AAA Lys	
CAG Gln	AAA Lys	CTT Leu	
AAA Lys	CTT Leu	CAG Gln	
CTT Leu	CAG Gln	TCT Ser	
CAG Gln	TCT Ser	CCA Pro	
TCT Ser	CCA Pro	GAC Asp 395	
CCA Pro	GAC Asp		
GAC Asp			
ATG Met	GGA Gly	GGC Gly	1309
GGA Gly	GGC Gly	AAT Asn 400	
GGC Gly	AAT Asn	GAG Glu	
AAT Asn	GAG Glu	TCC Ser	
GAG Glu	TCC Ser	AGC Ser	
TCC Ser	AGC Ser	ATC Ile	
AGC Ser	ATC Ile	TAC Tyr 405	
ATC Ile	TAC Tyr	TTC Phe	
TAC Tyr	TTC Phe	AGC Ser	
TTC Phe	AGC Ser	TGC Cys	
AGC Ser	TGC Cys	GTG Val 410	
TGC Cys	GTG Val	CAG Gln	
GTG Val	CAG Gln	AAA Lys	
CAG Gln	AAA Lys	TGC Cys	
AAA Lys	TGC Cys		

FIG. 16B

~~TAC TGC AAG CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA~~ 1357
 Tyr Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu
 415 420 425

~~CTG TCC ACC ATT ACT CTG CGA CTG GCC CGG TCC ACC CTG CTG CTC ATC~~ 1405
 Leu Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile
 430 435 440

CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA GAG AAT 1453
 Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn
 445 450 455 460

GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC 1501
 Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe
 465 470 475

CAG GGC TTT GTG GTG GCT GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA 1549
 Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val
 480 485 490

CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG GTG AAC CGT TAC 1597
 Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr
 495 500 505

TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG 1645
 Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly
 510 515 520

GTG AAT GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA 1693
 Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln
 525 530 535 540

ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT CTG GCC ACC TGAGCCATGC TCC 1745
 Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr
 545 550

CCT 1748

FIG. 16C

AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG	60
GCCAAGAAGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC	109
Met Ala Gly Val Val His Val Ser Leu Ala Ala His	
1 5 10	
TGC GGG GCC TGT CCG TGG GGC CGG GGC AGA CTC CGC AAA GGA CGC GCA	157
Cys Gly Ala Cys Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala	
15 20 25	
GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG	205
Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu	
30 35 40	
CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT	253
Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly	
45 50 55 60	
GTC GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT	301
Val Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro	
65 70 75	
GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG	349
Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu	
80 85 90	
GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT	397
Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser	
95 100 105	
CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC	445
Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala	
110 115 120	
CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC	493
His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile	
125 130 135 140	
TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT	541
Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp	
145 150 155	
TTT GGT GAC AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC	589
Phe Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser	
160 165 170	
CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA CCC TTC CCT CAT TAC TTT	637
Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe	
175 180 185	
GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT	685
Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp	
190 195 200	

FIG. 17A

TAT	TAC	TAC	CTG	TCA	GTG	AAG	GCC	CTC	TAC	ACG	GTT	GGC	TAC	AGC	ACA	733
Tyr	Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	
205					210					215					220	
TCC	CTC	GTC	ACC	CTC	ACC	ACT	GCC	ATG	GTC	ATC	CTT	TGT	CGC	TTC	CGG	781
Ser	Leu	Val	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	
				225					230					235		
AAG	CTG	CAC	TGC	ACA	CGC	AAC	TTC	ATC	CAC	ATG	AAC	CTG	TTT	GTG	TCG	829
Lys	Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	
			240					245					250			
TTC	ATG	CTG	AGG	GCG	ATC	TCC	GTC	TTC	ATC	AAA	GAC	TGG	ATT	CTG	TAT	877
Phe	Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	
		255					260					265				
GCG	GAG	CAG	GAC	AGC	AAC	CAC	TGC	TTC	ATC	TCC	ACT	GTG	GAA	TGT	AAG	925
Ala	Glu	Gln	Asp	Ser	Asn	His	Cys	Phe	Ile	Ser	Thr	Val	Glu	Cys	Lys	
	270					275					280					
GCC	GTC	ATG	GTT	TTC	TTC	CAC	TAC	TGT	GTT	GTG	TCC	AAC	TAC	TTC	TGG	973
Ala	Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	
285					290					295					300	
CTG	TTC	ATC	GAG	GGC	CTG	TAC	CTC	TTC	ACT	CTG	CTG	GTG	GAG	ACC	TTC	1021
Leu	Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	
				305					310					315		
TTC	CCT	GAA	AGG	AGA	TAC	TTC	TAC	TGG	TAC	ACC	ATC	ATT	GGC	TGG	GGG	1069
Phe	Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly	Trp	Gly	
			320					325					330			
ACC	CCA	ACT	GTG	TGT	GTG	ACA	GTG	TGG	GCT	ACG	CTG	AGA	CTC	TAC	TTT	1117
Thr	Pro	Thr	Val	Cys	Val	Thr	Val	Trp	Ala	Thr	Leu	Arg	Leu	Tyr	Phe	
			335				340					345				
GAT	GAC	ACA	GGC	TGC	TGG	GAT	ATG	AAT	GAC	AGC	ACA	GCT	CTG	TGG	TGG	1165
Asp	Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu	Trp	Trp	
		350				355					360					
GTG	ATC	AAA	GGC	CCT	GTG	GTT	GGC	TCT	ATC	ATG	GTT	AAC	TTT	GTG	CTT	1213
Val	Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	
365					370					375				380		
TTT	ATT	GGC	ATT	ATC	GTC	ATC	CTT	GTG	CAG	AAA	CTT	CAG	TCT	CCA	GAC	1261
Phe	Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	
				385					390					395		
ATG	GGA	GGC	AAT	GAG	TCC	AGC	ATC	TAC	TTC	TGC	GTG	CAG	AAA	TGC	TAC	1309
Met	Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Cys	Val	Gln	Lys	Cys	Tyr	
			400				405					410				
TGC	AAG	CCA	CAG	CGG	GCT	CAG	CAG	CAC	TCT	TGC	AAG	ATG	TCA	GAA	CTG	1357
Cys	Lys	Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	

FIG. 17B

415					420					425						
TCC	ACC	ATT	ACT	CTG	CGA	CTG	GCC	CGG	TCC	ACC	CTG	CTG	CTC	ATC	CCA	1405
Ser	Thr	Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro	
	430					435					440					
CTA	TTC	GGA	ATC	CAC	TAC	ACA	GTA	TTT	GCC	TTC	TCC	CCA	GAG	AAT	GTC	1453
Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro	Glu	Asn	Val	
445					450					455					460	
AGC	AAA	AGG	GAA	AGA	CTC	GTG	TTT	GAG	CTG	GGG	CTG	GGC	TCC	TTC	CAG	1501
Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	Gly	Ser	Phe	Gln	
				465					470					475		
GGC	TTT	GTG	GTG	GCT	GTT	CTC	TAC	TGT	TTT	CTG	AAT	GGT	GAG	GTA	CAA	1549
Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn	Gly	Glu	Val	Gln	
			480					485					490			
GCG	GAG	ATC	AAG	CGA	AAA	TGG	CGA	AGC	TGG	AAG	GTG	AAC	CGT	TAC	TTC	1597
Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	Asn	Arg	Tyr	Phe	
		495					500					505				
GCT	GTG	GAC	TTC	AAG	CAC	CGA	CAC	CCG	TCT	CTG	GCC	AGC	AGT	GGG	GTG	1645
Ala	Val	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala	Ser	Ser	Gly	Val	
	510					515					520					
AAT	GGG	GGC	ACC	CAG	CTC	TCC	ATC	CTG	AGC	AAG	AGC	AGC	TCC	CAA	ATC	1693
Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser	Ser	Ser	Gln	Ile	
525					530					535					540	
CGC	ATG	TCT	GGC	CTC	CCT	GCT	GAC	AAT	CTG	GCC	ACC	TGAGCCATGC	TCCCCT			1745
Arg	Met	Ser	Gly	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr	***				
				545					550							

FIG. 17C

AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG	60
GCCAAGAAGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC	109
Met Ala Gly Val Val His Val Ser Leu Ala Ala His	
1 5 10	
TGC GGG GCC TGT CCG TGG GGC CGG GGC AGA CTC CGC AAA GGA CGC GCA	157
Cys Gly Ala Cys Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala	
15 20 25	
GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG	205
Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu	
30 35 40	
CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT	253
Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly	
45 50 55 60	
GTC GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT	301
Val Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro	
65 70 75	
GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG	349
Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu	
80 85 90	
GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT	397
Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser	
95 100 105	
CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC	445
Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala	
110 115 120	
CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC	493
His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile	
125 130 135 140	
TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT	541
Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp	
145 150 155	
TTT GGT GAC AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC	589
Phe Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser	
160 165 170	
CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA CCC TTC CCT CAT TAC TTT	637
Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe	
175 180 185	
GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT	685
Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp	

FIG. 18A

190	195	200	
TAT TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr 205 210 215 220			733
TCC CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTT TGT CGC TTC CGG Ser Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg 225 230 235			781
AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG TCG Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser 240 245 250			829
TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr 255 260 265			877
GCG GAG CAG GAC AGC AAC CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG Ala Glu Gln Asp Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys 270 275 280			925
GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC TAC TTC TGG Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp 285 290 295 300			973
CTG TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe 305 310 315			1021
TTC CCT GAA AGG AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly 320 325 330			1069
ACC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG CTG AGA CTC TAC TTT Thr Pro Thr Val Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe 335 340 345			1117
GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT CTG TGG TGG Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp 350 355 360			1165
GTG ATC AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT Val Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu 365 370 375 380			1213
TTT ATT GGC ATT ATC GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp 385 390 395			1261
ATG GGA GGC AAT GAG TCC AGC ATC TAC TTA ACA AAT TTA AGC CCG CGA Met Gly Gly Asn Glu Ser Ser Ile Tyr Leu Thr Asn Leu Ser Pro Arg 400 405 410			1309

FIG. 18B

GTC CCC AAG AAA GCC CGA GAG GAC CCC CTG CCT GTG CCC TCA GAC CAG	1357
Val Pro Lys Lys Ala Arg Glu Asp Pro Leu Pro Val Pro Ser Asp Gln	
415 420 425	
CAT TCA CTC CCT TTC CTG CGA CTG GCC CGG TCC ACC CTG CTG CTC ATC	1405
His Ser Leu Pro Phe Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile	
430 435 440	
CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA GAG AAT	1453
Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn	
445 450 455 460	
GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC	1501
Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe	
465 470 475	
CAG GGC TTT GTG GTG GCT GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA	1549
Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val	
480 485 490	
CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG GTG AAC CGT TAC	1597
Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr	
495 500 505	
TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG	1645
Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly	
510 515 520	
GTG AAT GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA	1693
Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln	
525 530 535 540	
ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT CTG GCC ACC TGAGCCATGC TCC	1745
Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr ***	
545 550	
CCT	1748

FIG. 18C

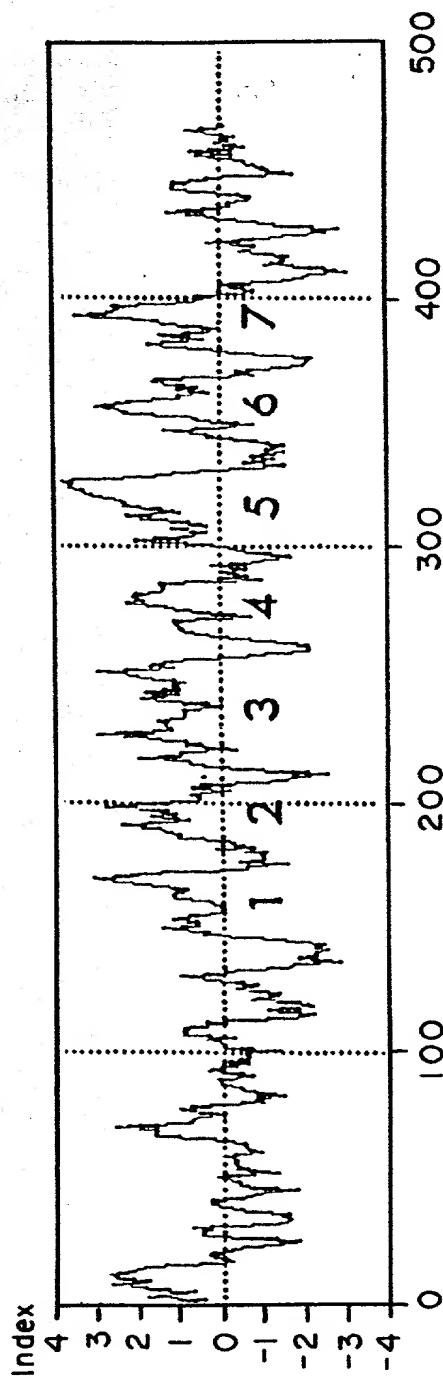


FIG. 19A

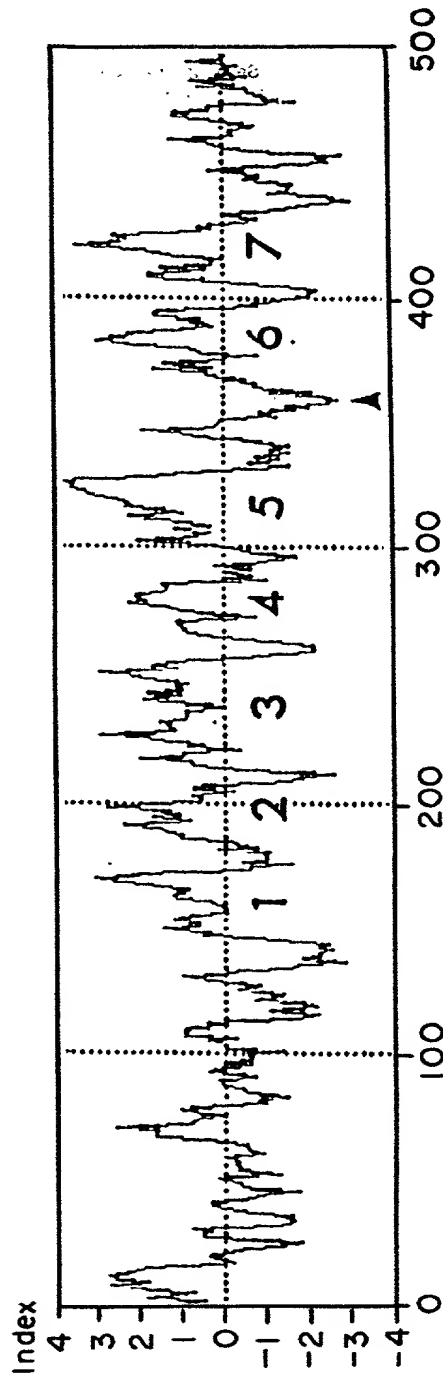


FIG. 19B

19	29	39	49	59	69	79
TALLLPVAIAMHSDCIFKKEQAMCLERIQRANDLMGLNESSPGCPGMWDNITCWKPAQVGEMVLVSCPEV						
* *	**	* *	*	* *	* *	**
MRPPSPPHVRWLCVLAGALACALRPAGSQAASPOHECEYLQLIEIQRQQCLEEAQLENETTGCCKMWDNL						
10	20	30	40	50	60	70
89	99	109	119	129	139	149
FRIFNPQVWMTETIGDSGFADSNLEITDMGVVGRNCTEDGWSEPFPHYFDACGFDDYEPESGDQDYYY						
*	*	**	***	* *	* *	* **
TCWPTTPRGQAVVLDCLIFQLFAPIHGYNISRSCTEEGWSQLEPGPYHIACGLNDRASSLDEQQQTKFY						
80	90	100	110	120	130	140
159	169	179	189	199	209	219
LSVKALYTVGYSTSLATLTAMVILCRFRKLHCTRNIHMNLFVSFMLRAISVFIKDWILYAEQDSSHCF						
****	*****	*****	** **	*****	*****	** *
NTVKTYGTIGYSLASLLVAMAILSLFRKLHCTRNYIHMHLFMSFILRATAVFIKDMALFNSGEIDHCS						
150	160	170	180	190	200	210
229	239	249	259	269	279	289
VSTVECKAVMVFFHYCVVSNYFWLFIIEGLYLFLLVETFFPERRYFYWYTIIGWGTPTVCVTWAVLRLY						
***	***	*****	*****	*****	* *****	*** *****
EASVGCKAAVVFQYCVMANFFWLLVEGLYLYTLLAVSFFSERKYFWGYILIGWGVPSVFITIWTVVRIY						
220	230	240	250	260	270	280
299	309	319	329	339	349	359
FDDAGCWDMDSTALWWIKGPVVGSI MNFVLFIGIIILVQKLQSPDMGGNESSIYLRARSTLLIP						
***	***	*****	*****	** *****	*****	* *****
FEDFGCWDTIINSSLWWIIKAPILLSILVNFVLFICIIRILVQKLRPDPDIGKNDSSPYSRLAKSTLLIP						
290	300	310	320	330	340	350
369	379	389	399	409	419	429
LFGIHYTVFAFSPENVSKRERLVFELGLGSFQGFVAVLYCFLNGEVQAEIKRKWRSWKVNRYFTMDFKH						
*****	***	*****	*****	*****	*****	* *
LFGIHYVMFAFFPDNFKAQVKMFELVVGFSQGFVAVLYCFLNGEVQAEILRRKWRRWHLQGVLGWSSKS						
360	370	380	390	400	410	420
439	449	459				
RHPSLASSGVNGGTQLSILSKSSSQLRMSSLPADNLAT*						
**	** *	*****	**	* **	***	
QHPWGSNGATCSTQVSMLTRVSPSARRSSSFQAEVSLV						
430	440	450				

FIG.20

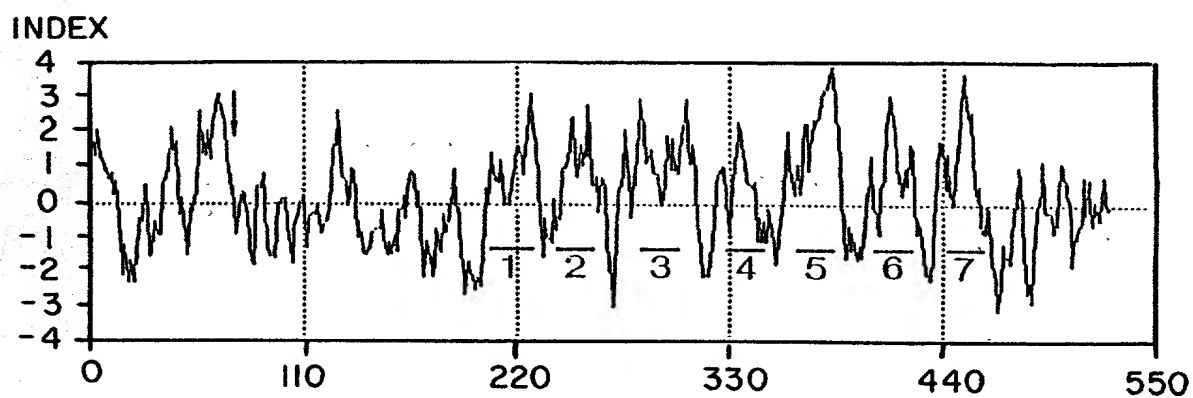


FIG. 21

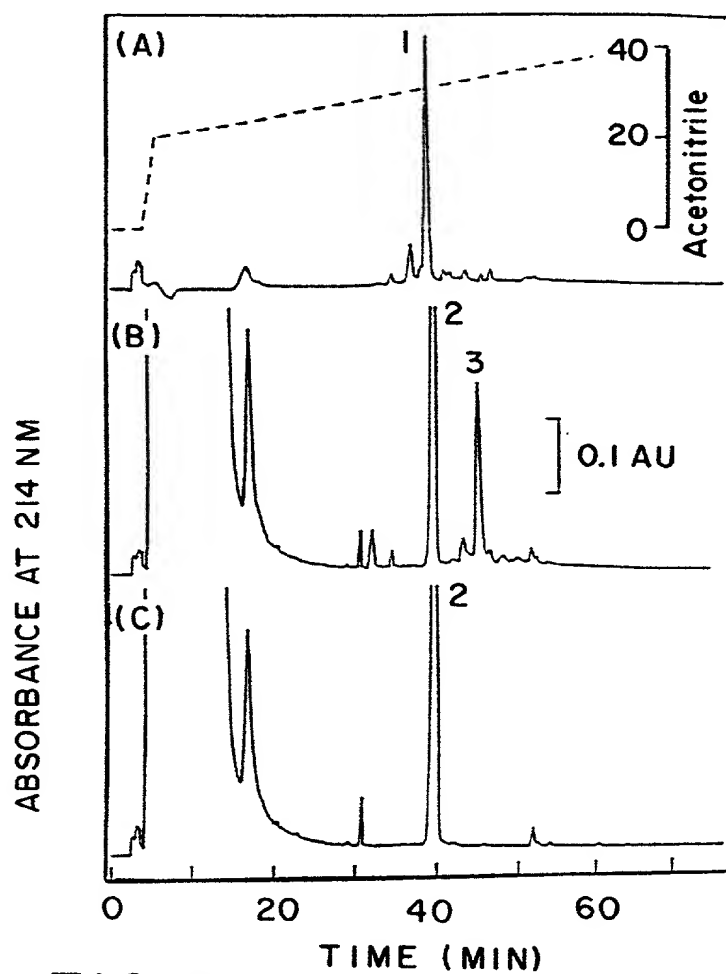


FIG. 28

	10	20	30	40	50	60	70	80
HUMAN	MAGVHVSLA	AHCGACPWGR	GRLRKGRAAC	KSAAQRHIGA	DLPLLSVGGQ	WQPRSVMAG	WVHVSIAALL	LLPMAFAMHS
BOVINE	MRGGRHMEPEP	PQRLRVSMAS	IAQVSLAALL	LLPMAFAMHS
RAT
	90	100	110	120	130	140	150	160
	DCIFKKEQAM	CLEKIQORANE	LMGENDSSPG	CPGMNDNITC	WKPAHVGEV	LVSCPELFRI	FNPQVWETE	TIGESDFGDS
	DCIFKKEQAM	CLEKIQORVND	LMGLNDSSPG	CPGMNDNITC	WKPAHVGEV	LVSCPELFRI	FNPQVWETE	TIGEFJGFADS
	DCIFKKEQAM	CLEKIQORAND	LMGLNFSSPG	CPGMNDNITC	WKPAHVGEV	LVSCPELFRI	FNPQVWETE	TIGDSGFADS
	170	180	190	200	210	220	230	240
	NSLDLSDMGV	VSRLCTEDGW	SEPFPHYFDA	CGFDEYESET	GQDQVYVLSV	KALYTVGYST	SLVTLTTAMV	ILCRFRKLHC
	NSLDLSDMGV	VSRLCTEDGW	SEPFPHYFDA	CGFDEYESET	GQDQVYVLSV	KALYTVGYST	SLVTLTTAMV	ILCRFRKLHC
	NSLEITDMGV	VSRLCTEDGW	SEPFPHYFDA	CGFDEYESET	GQDQVYVLSV	KALYTVGYST	SLVTLTTAMV	ILCRFRKLHC
	250	260	270	280	290	300	310	320
	TRNFIHMNLF	VSFMLRAISV	FIKDWILYAE	QDSNHCFVST	VECKAVMVFF	HYCVWSNYFW	LFIEGLYLFT	LLVETFFPER
	TRNFIHMNLF	VSFMLRAISV	FIKDWILYAE	QDSNHCFVST	VECKAVMVFF	HYCVWSNYFW	LFIEGLYLFT	LLVETFFPER
	TRNFIHMNLF	VSFMLRAISV	FIKDWILYAE	QDSNHCFVST	VECKAVMVFF	HYCVWSNYFW	LFIEGLYLFT	LLVETFFPER
	330	340	350	360	370	380	390	400
	RYFYWYTIIG	WGTPTVCVTV	WALRLRYFDD	TGCDMDNDST	ALWVWIKGPV	VGSIMWNFVL	FIGIIVILVQ	KLOSPDMGGN
	RYFYWYTIIG	WGTPTVCVTV	WALRLRYFDD	TGCDMDNDST	ALWVWIKGPV	VGSIMWNFVL	FIGIIVILVQ	KLOSPDMGGN
	RYFYWYTIIG	WGTPTVCVTV	WALRLRYFDD	TGCDMDNDST	ALWVWIKGPV	VGSIMWNFVL	FIGIIVILVQ	KLOSPDMGGN
	410	420	430	440	450	460	470	480
	ESSIY-----	-----	-----	-----	-----	-----	-----	-----
	ESSIYFSCVQ	KCYCKPQRAQ	QHSCKMSELS	TITLRLARST	LLLIPLEFGIH	YTVFAFSPEN	VSKRERLVFE	LGLGSFQGFV
	ESSIYFSCVQ	KCYCKPQRAQ	QHSCKMSELS	TITLRLARST	LLLIPLEFGIH	YTVFAFSPEN	VSKRERLVFE	LGLGSFQGFV
	ESSIYFSCVQ	KCYCKPQRAQ	QHSCKMSELS	TITLRLARST	LLLIPLEFGIH	YTVFAFSPEN	VSKRERLVFE	LGLGSFQGFV
	490	500	510	520	530	540	550	
	VAVLYCFLNG	EVOAEIKRKW	RSWKVNRYFA	MDFKHRHPSL	ASSGVNGGTQ	LSILSKSSQ	IRMSGLPADN	LAT
	VAVLYCFLNG	EVOAEIKRKW	RSWKVNRYFT	MDFKHRHPSL	ASSGVNGGTQ	LSILSKSSQ	IRMSGLPADN	LAT
	VAVLYCFLNG	EVOAEIKRKW	RSWKVNRYFT	MDFKHRHPSL	ASSGVNGGTQ	LSILSKSSQ	IRMSGLPADN	LAT

FIG. 22

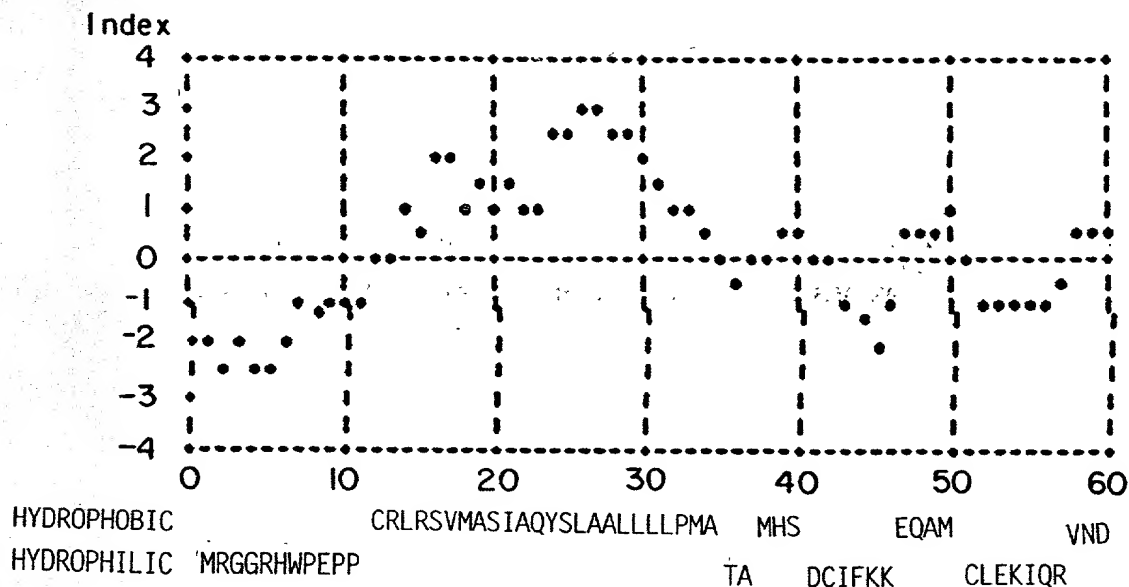


FIG. 23A

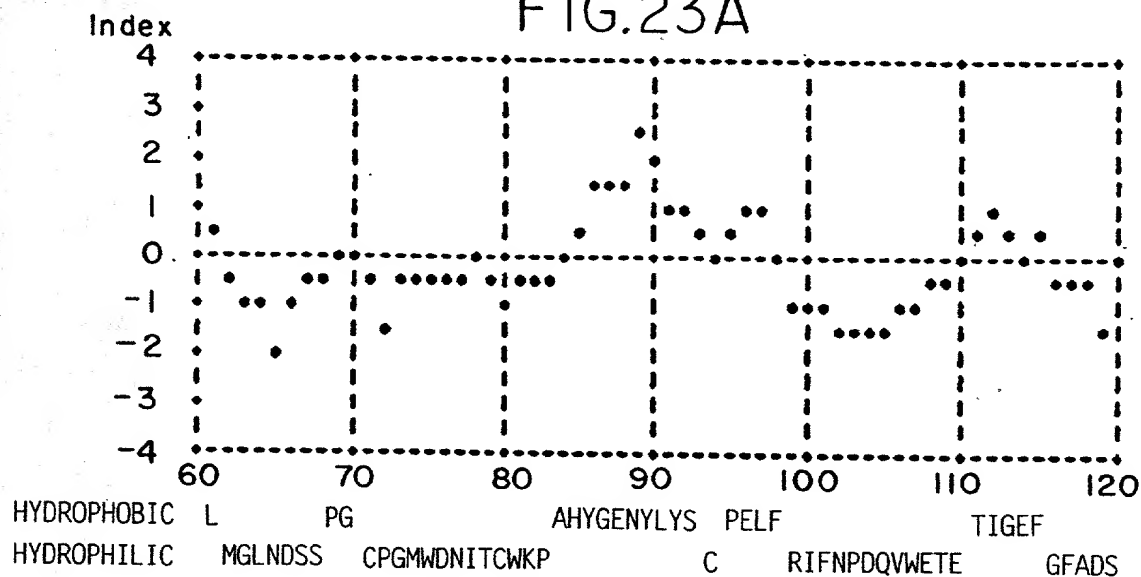


FIG. 23B

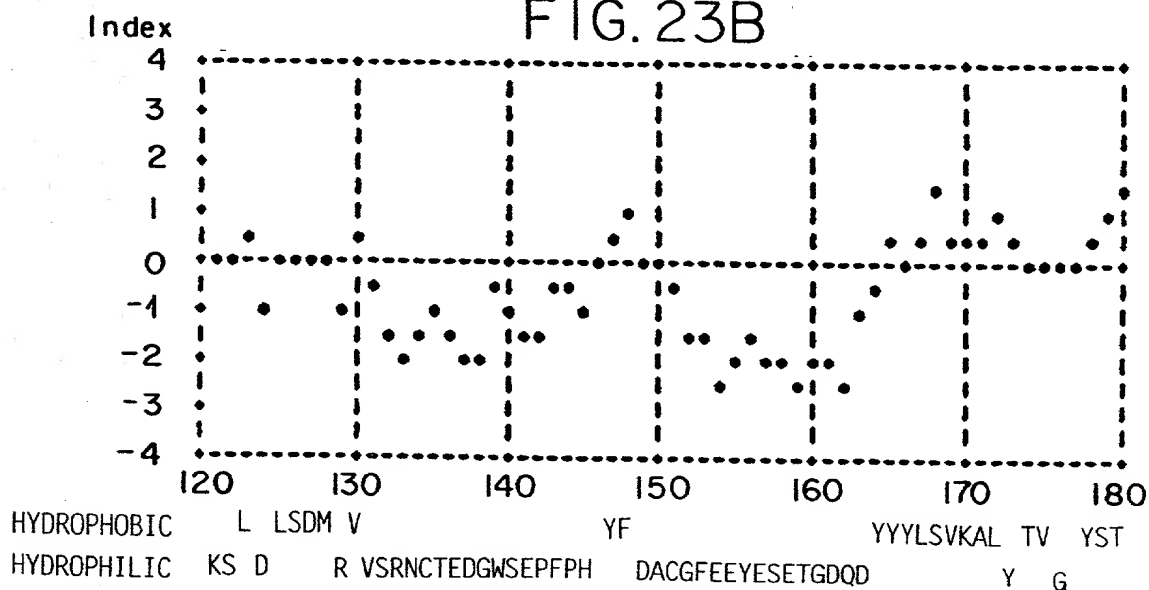


FIG. 23C

COPY OF
ORIGINAL

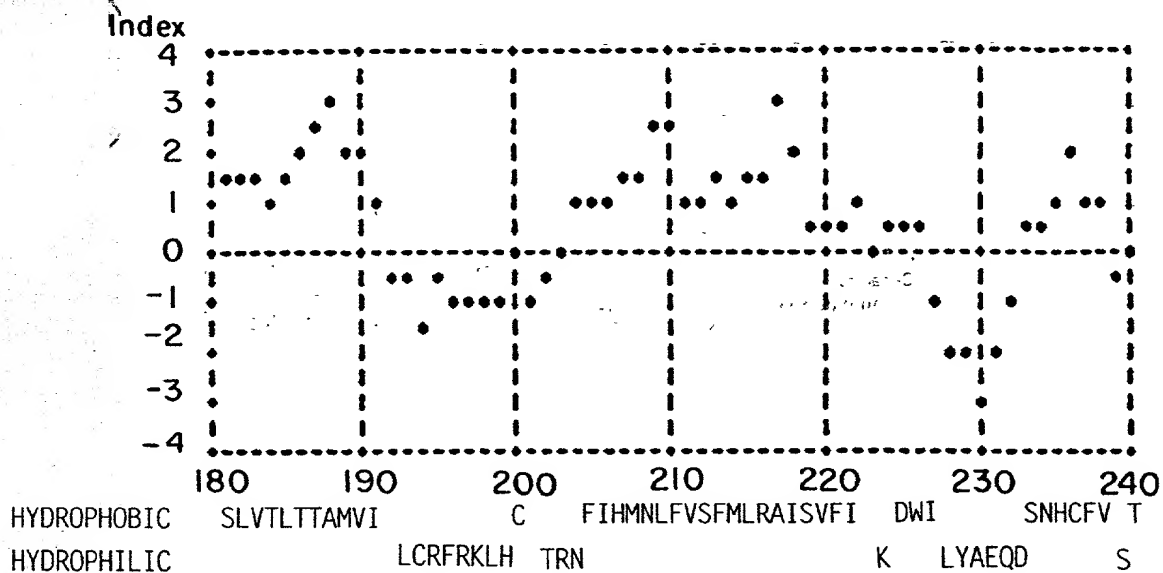


FIG. 23D

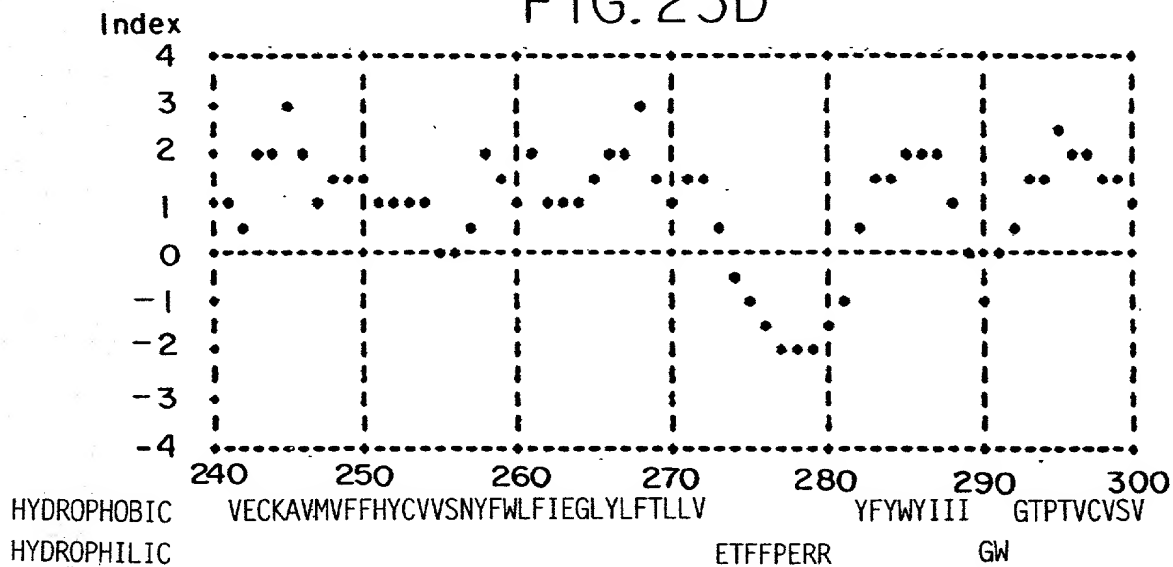


FIG. 23E

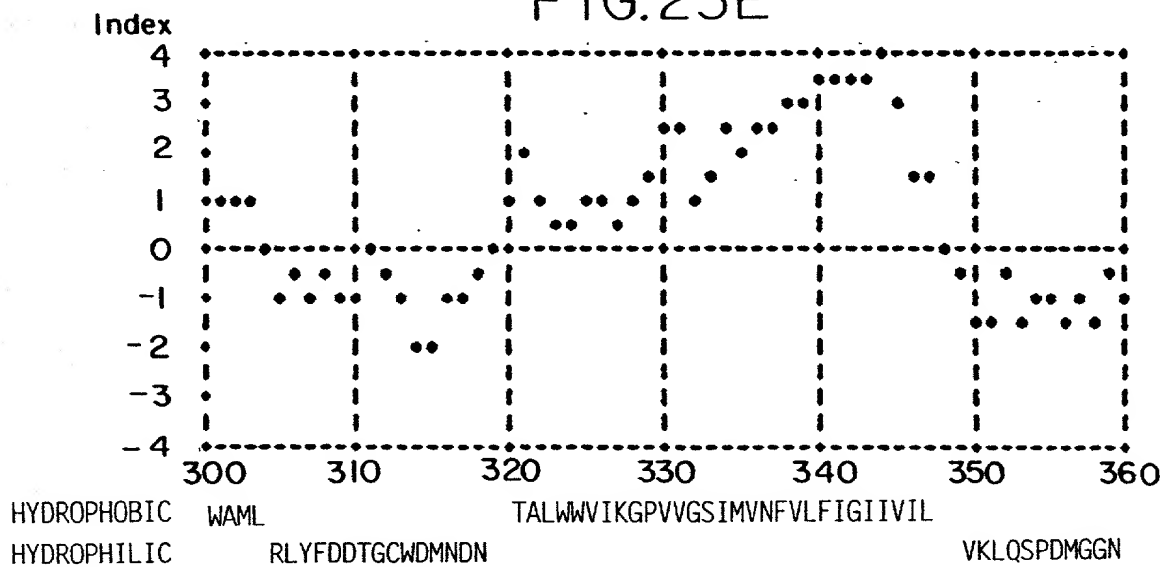


FIG. 23F

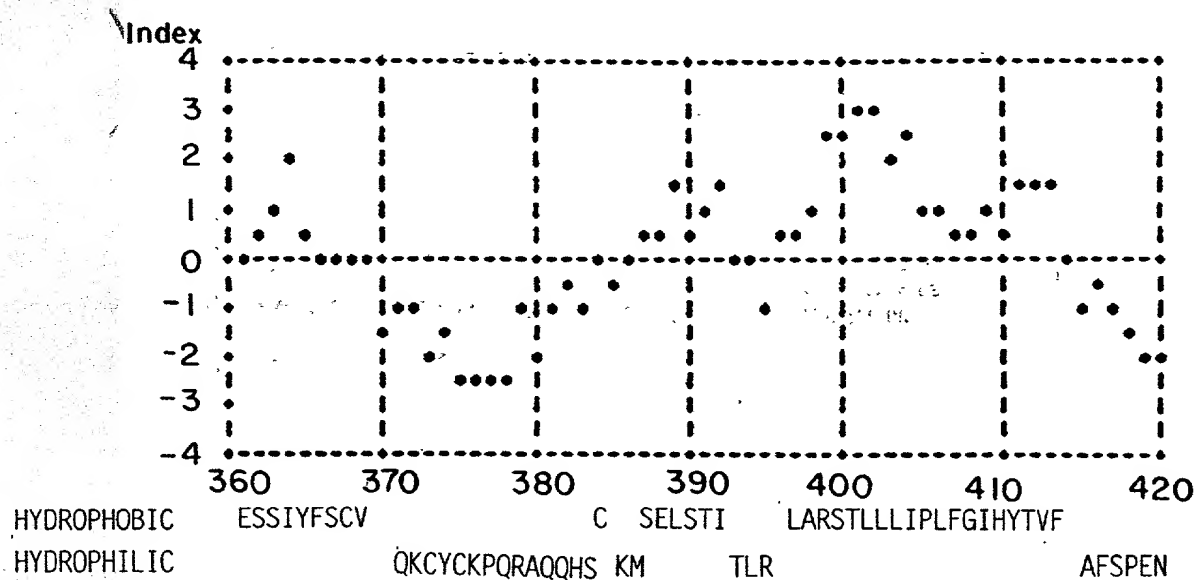


FIG.23G

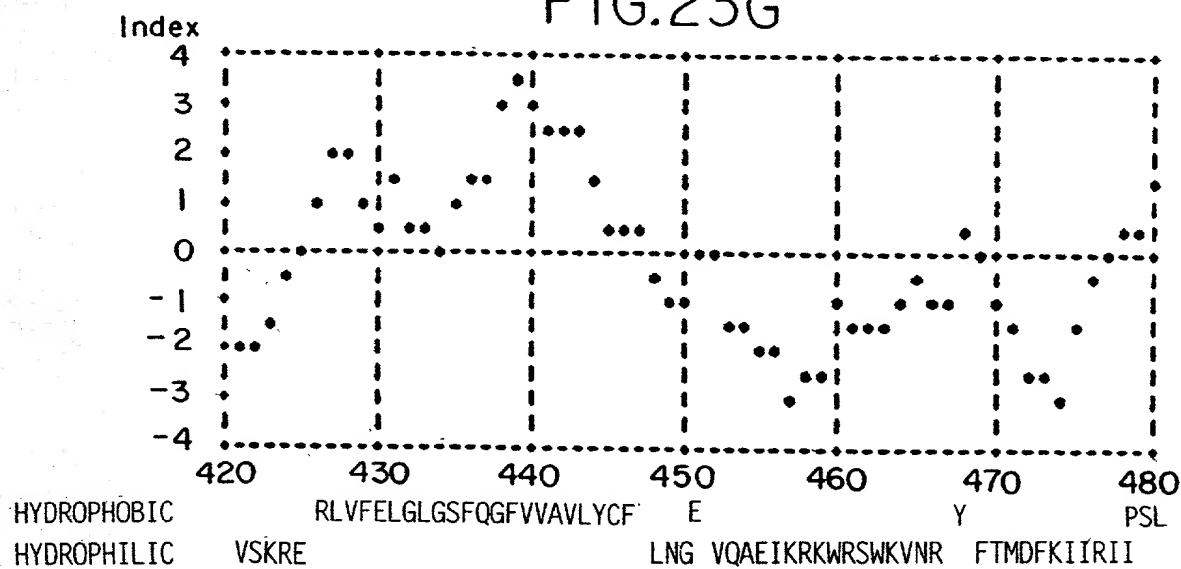


FIG.23H

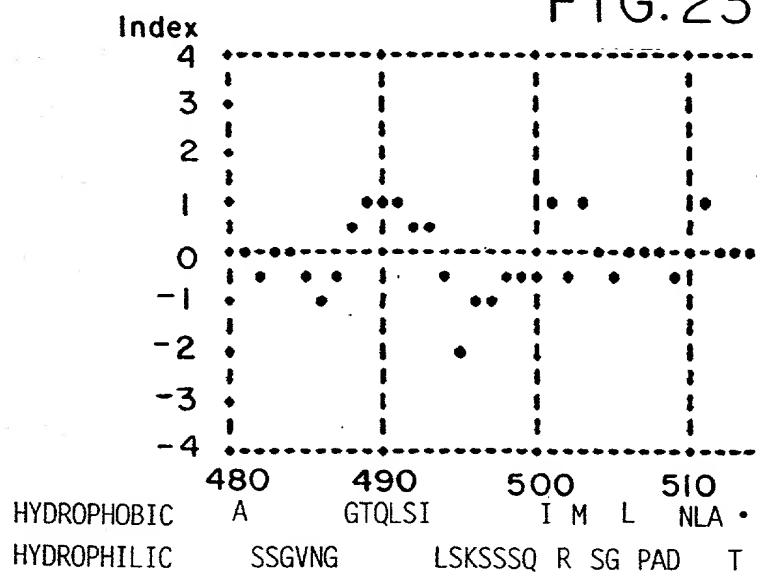


FIG.23I

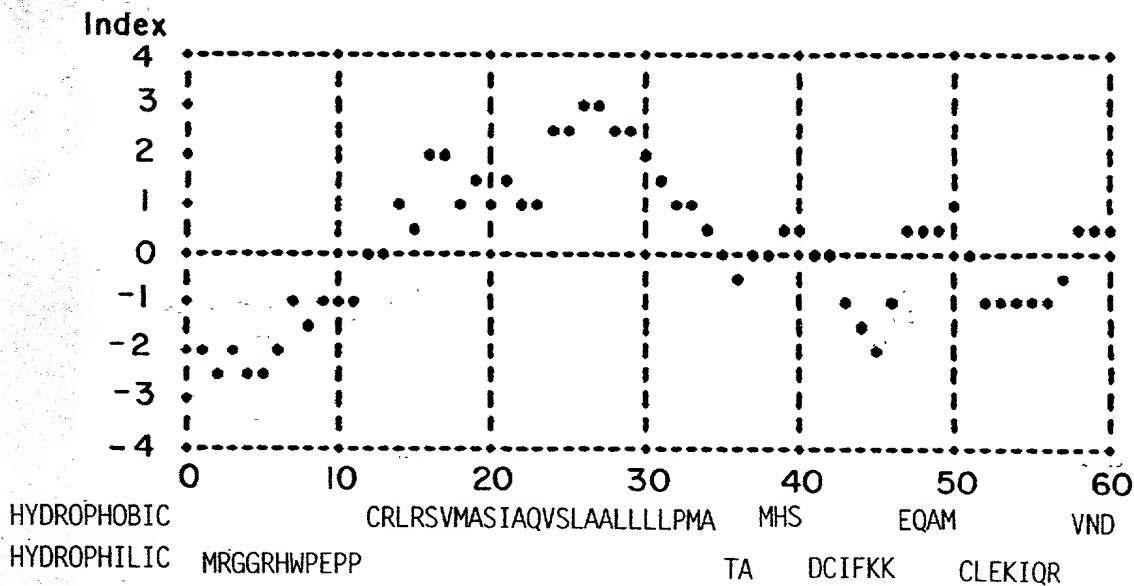


FIG.24A

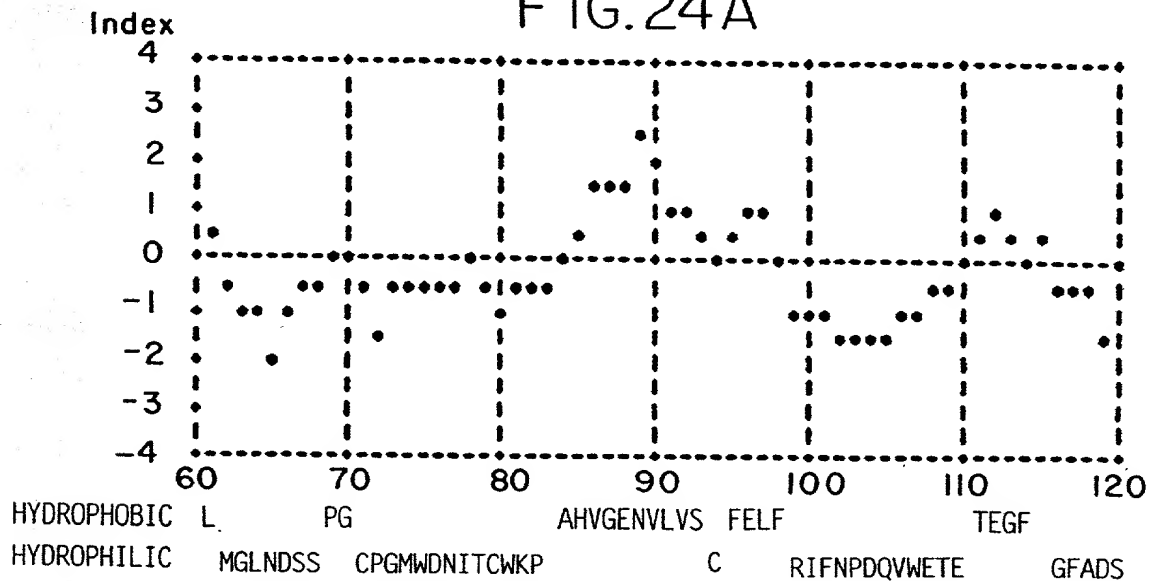


FIG.24B

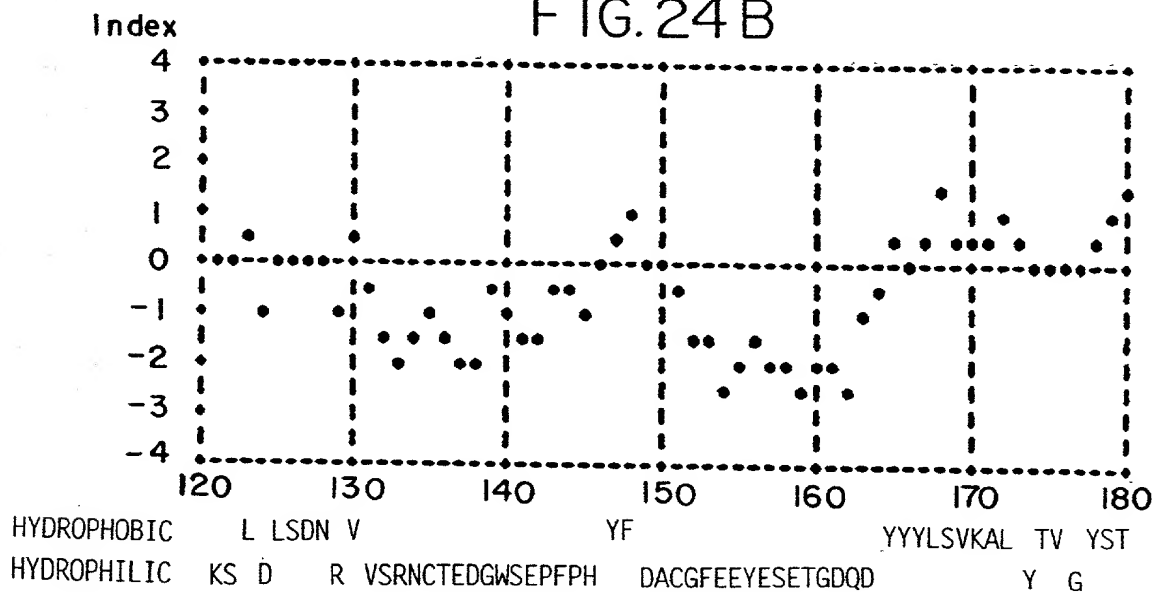


FIG.24C

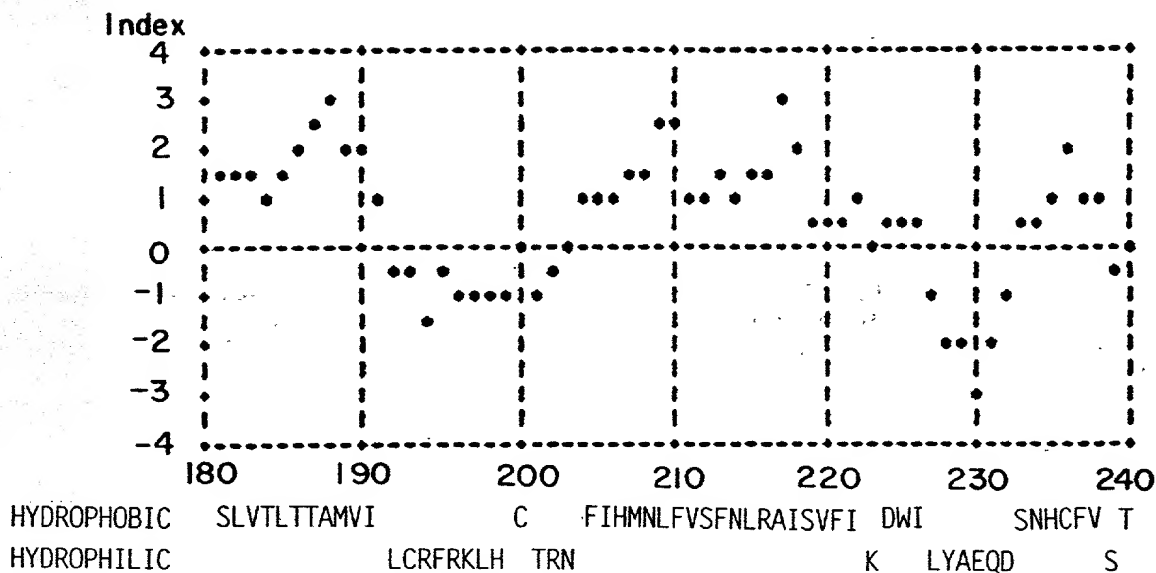


FIG. 24D

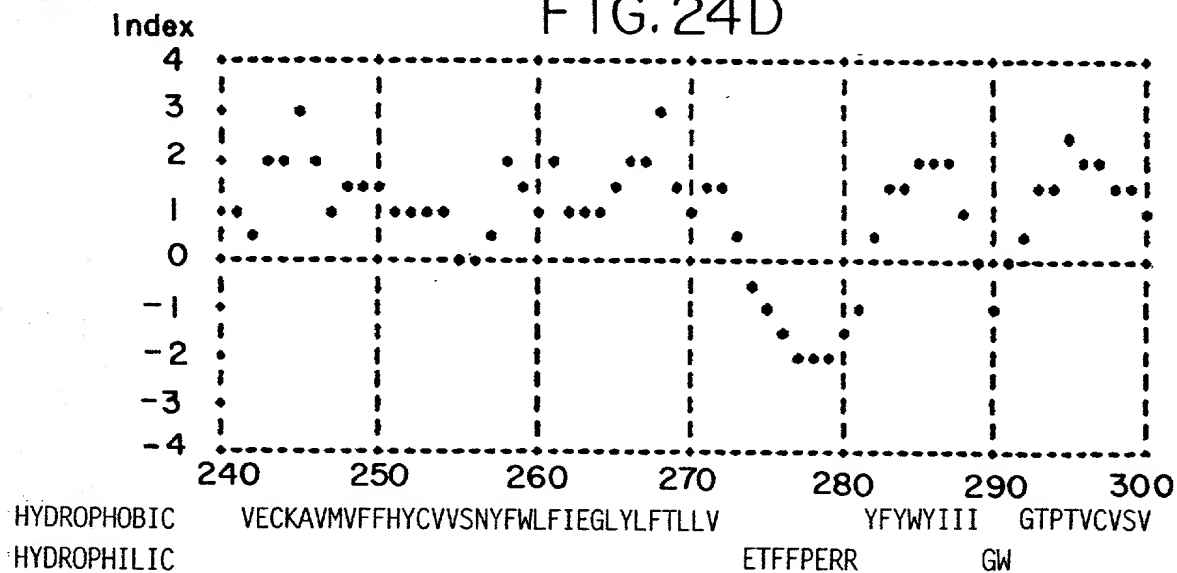


FIG. 24E

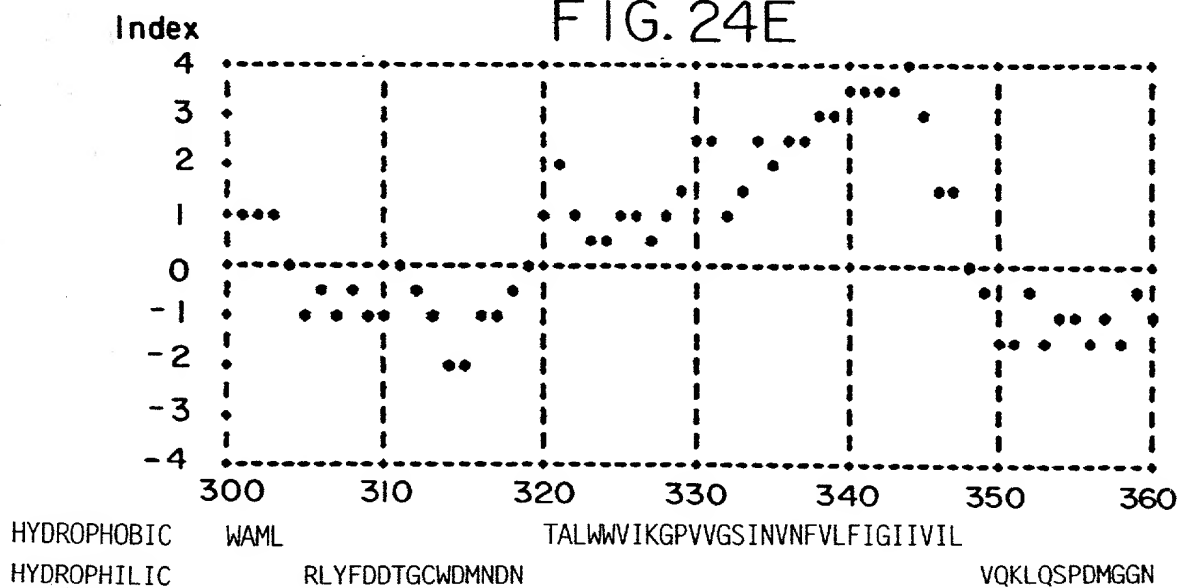


FIG. 24F

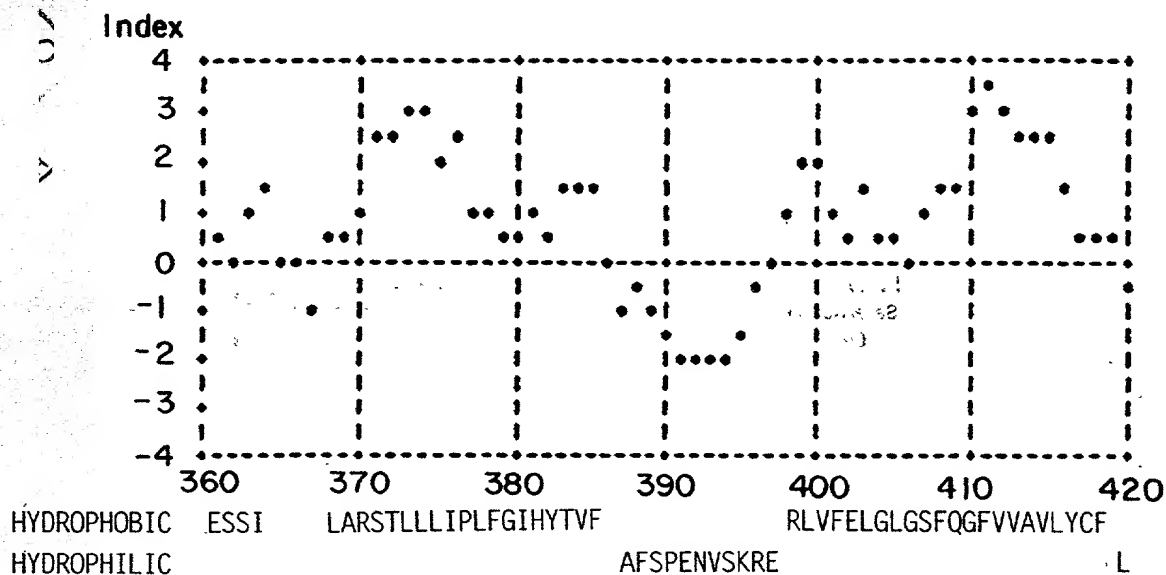


FIG. 24G

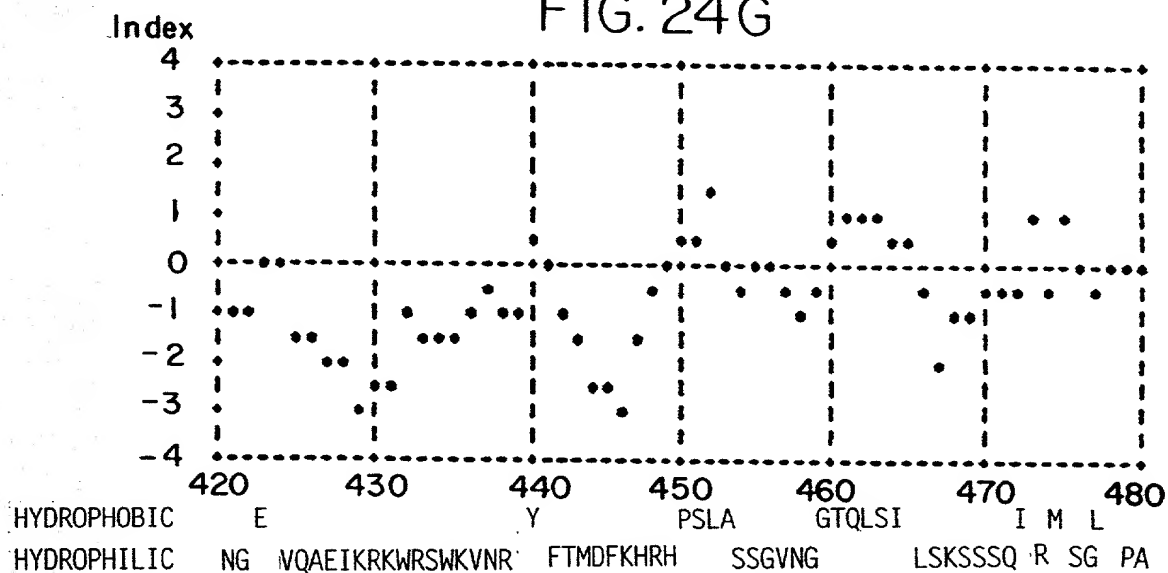


FIG. 24H

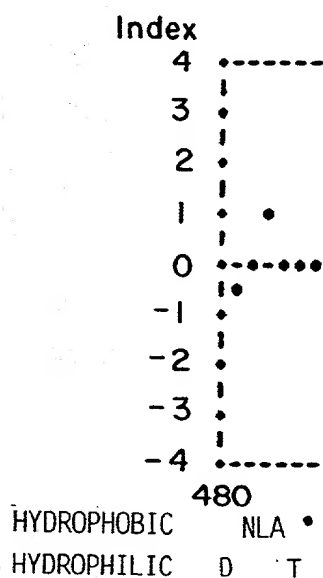


FIG. 24I

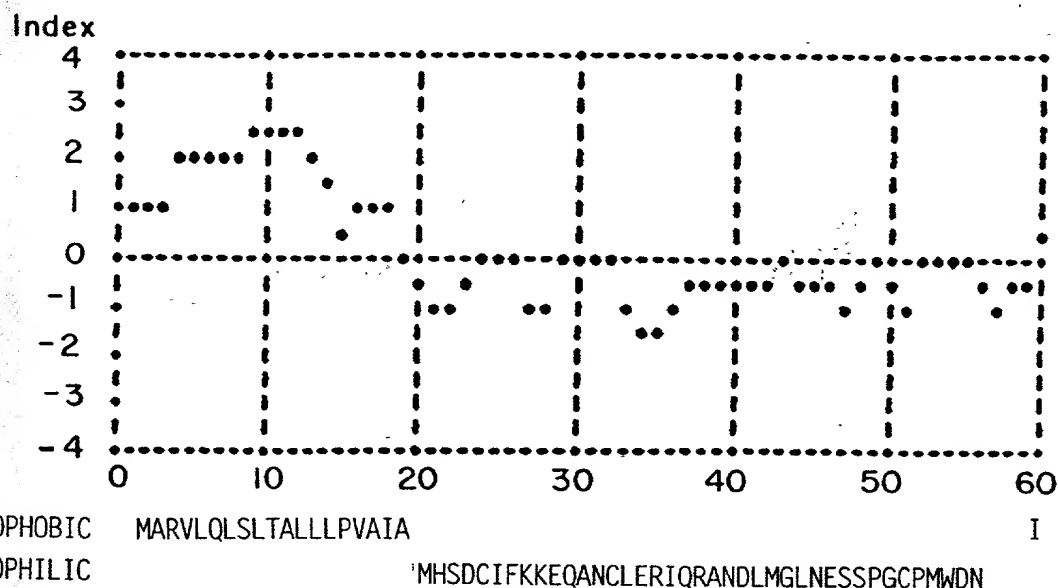


FIG.25A

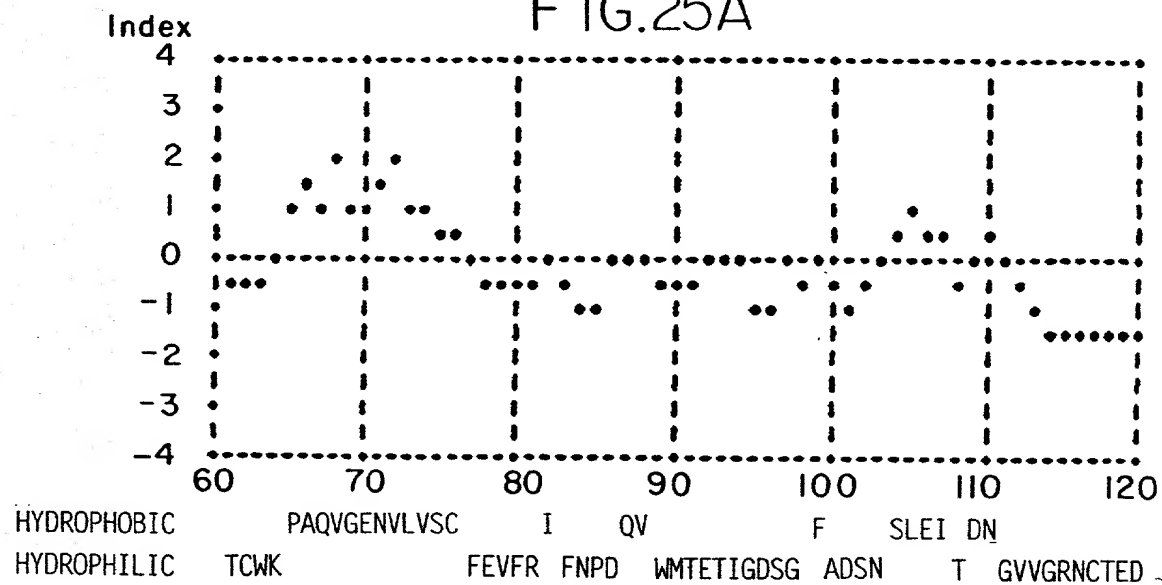


FIG.25B

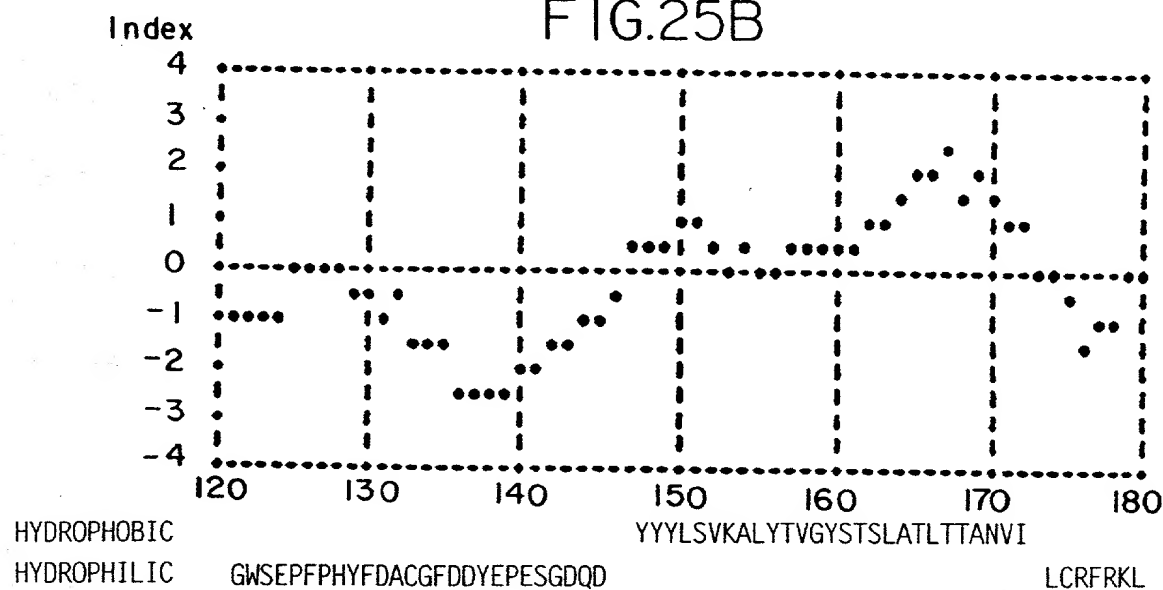


FIG.25C

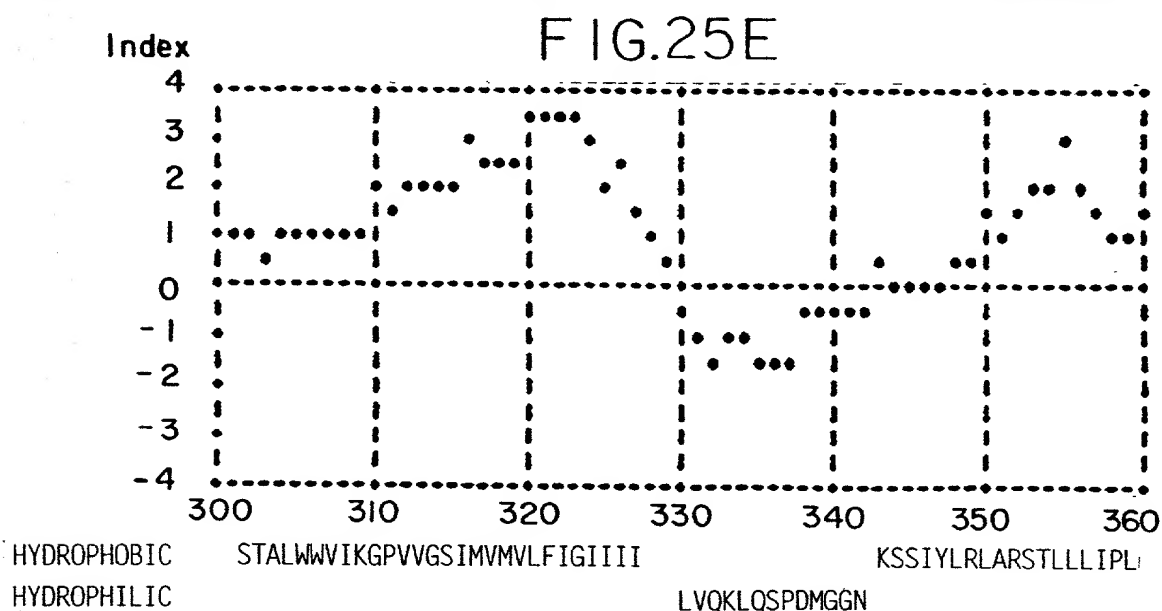
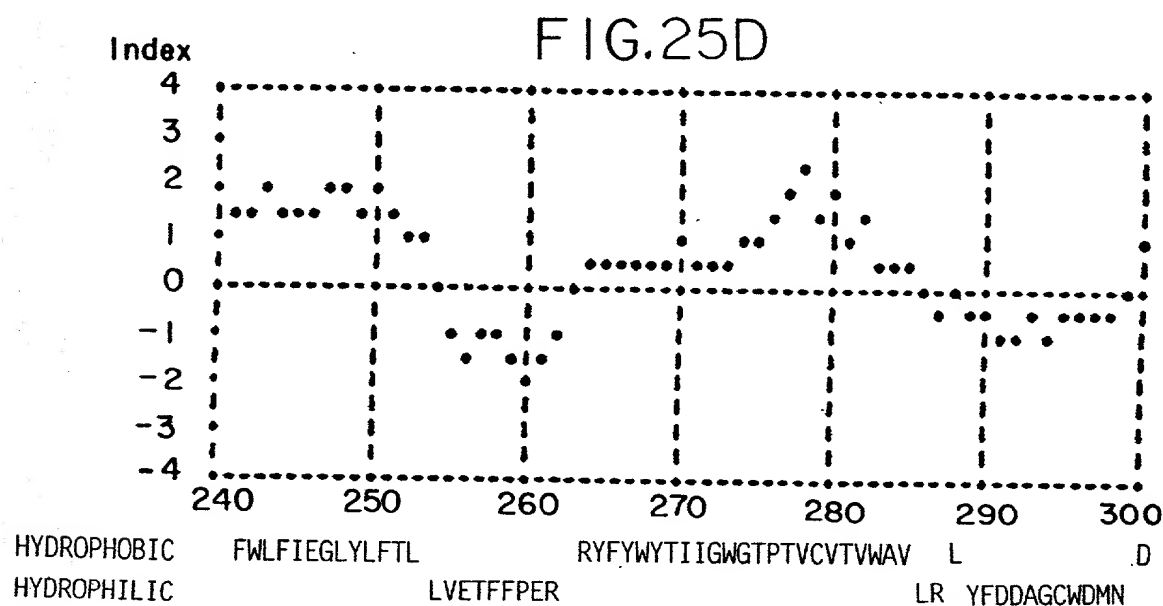
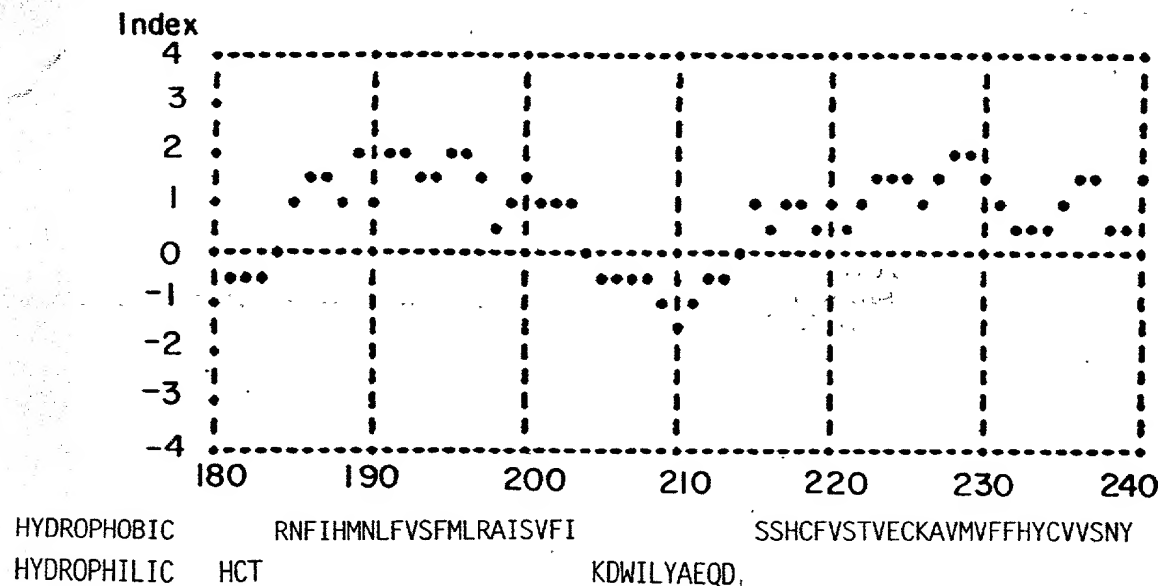
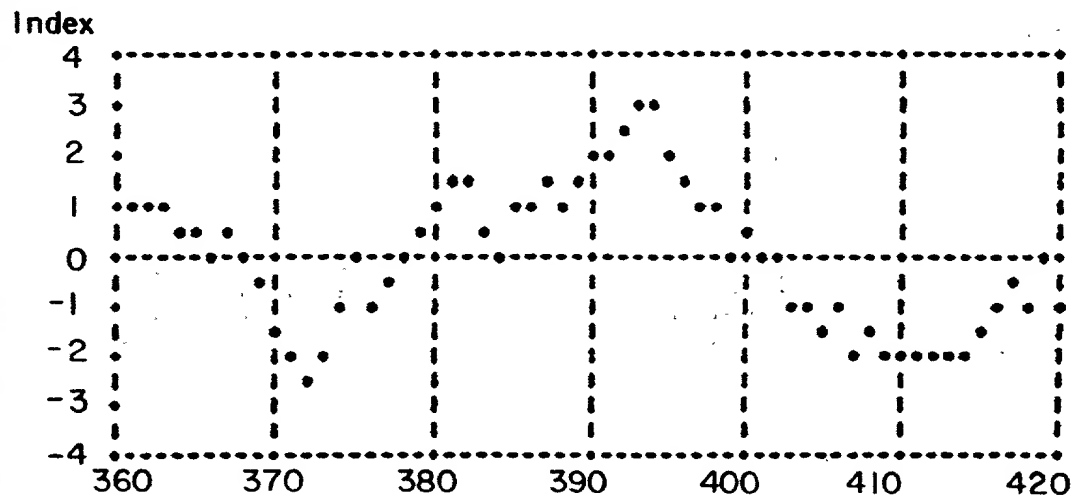


FIG.25F



HYDROPHOBIC
HYDROPHILIC

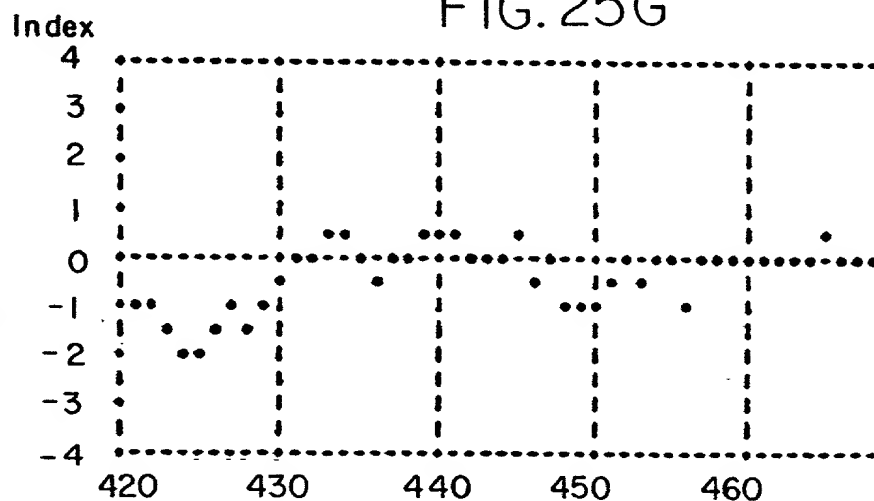
FGIHTYVF

ERLVEFELGLGSFQGFVVAVLYC

AFSPENVSKR

FLNGEVQAEIKKKWRSWKVN

FIG. 25G



HYDROPHOBIC
HYDROPHILIC

RYFTMDFKHR

ASSG

LSKSSS

R

PAD T

FIG. 25H

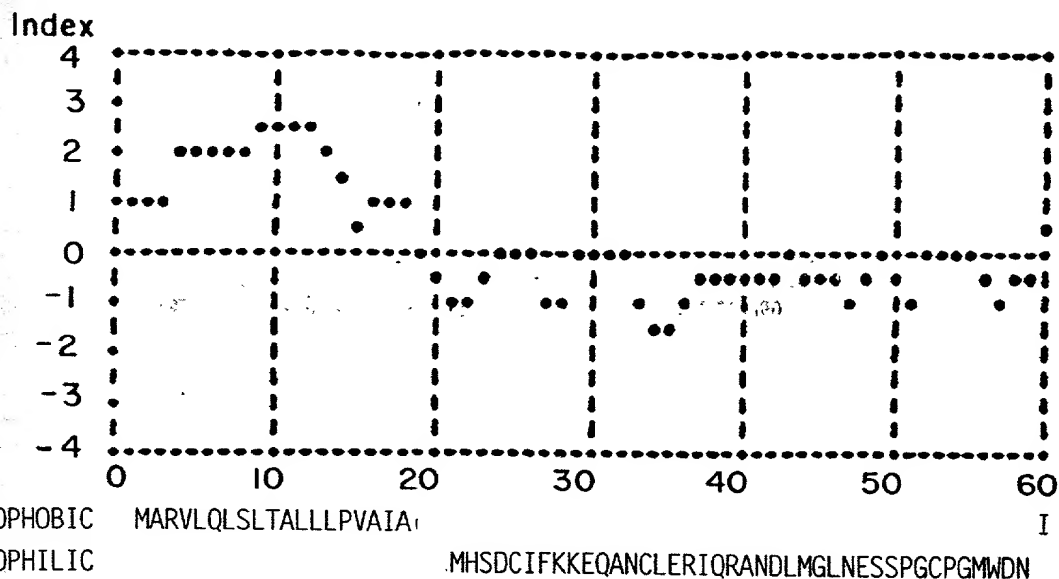


FIG.26A

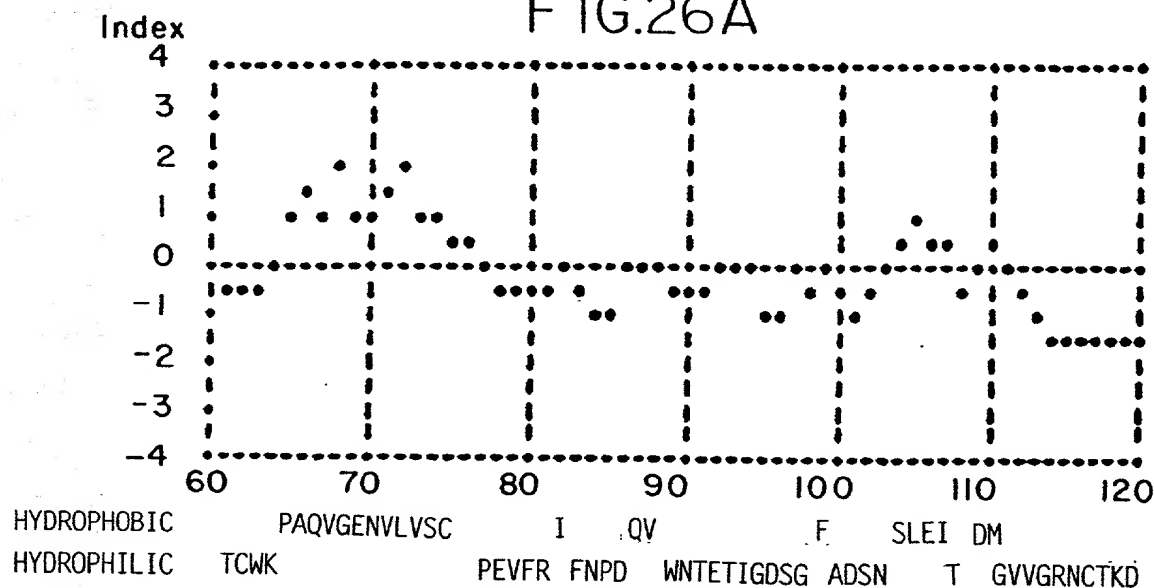


FIG.26B

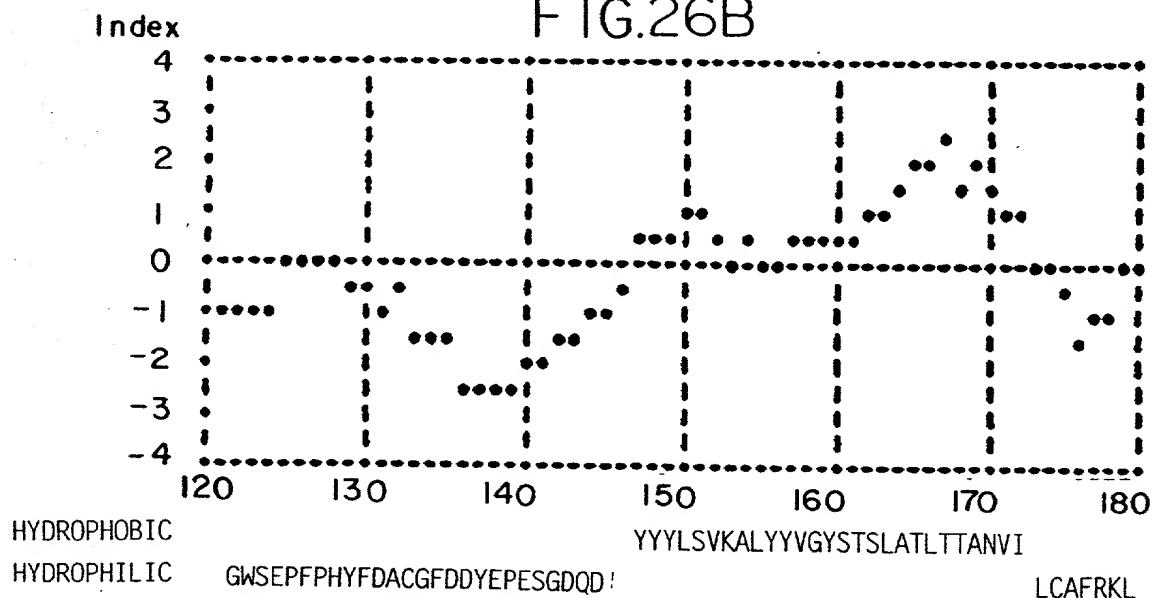


FIG.26C

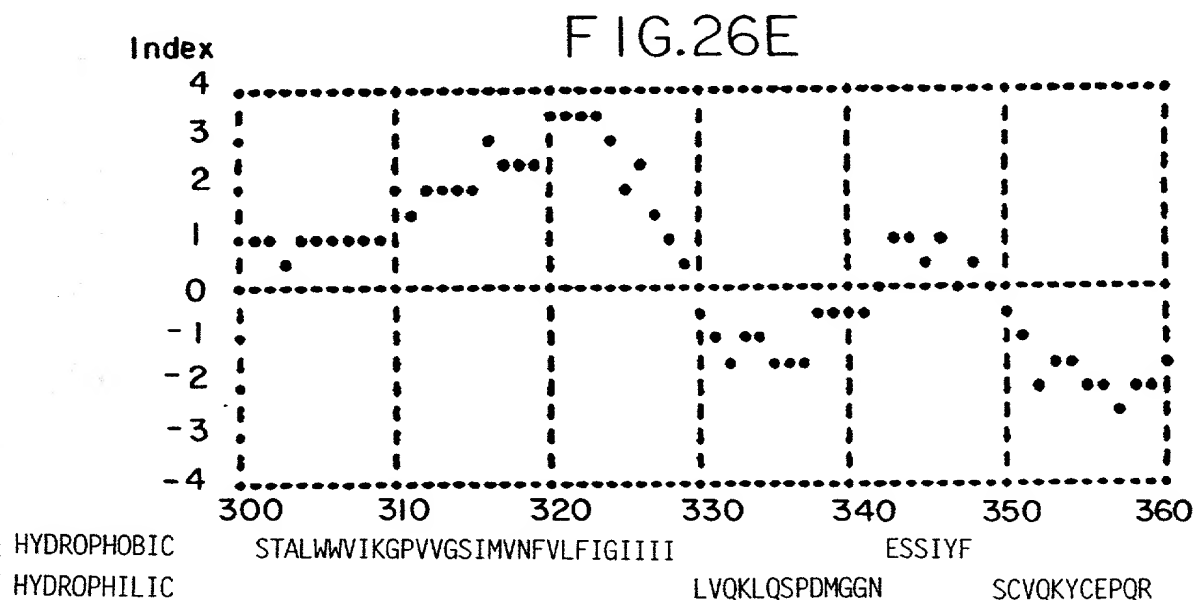
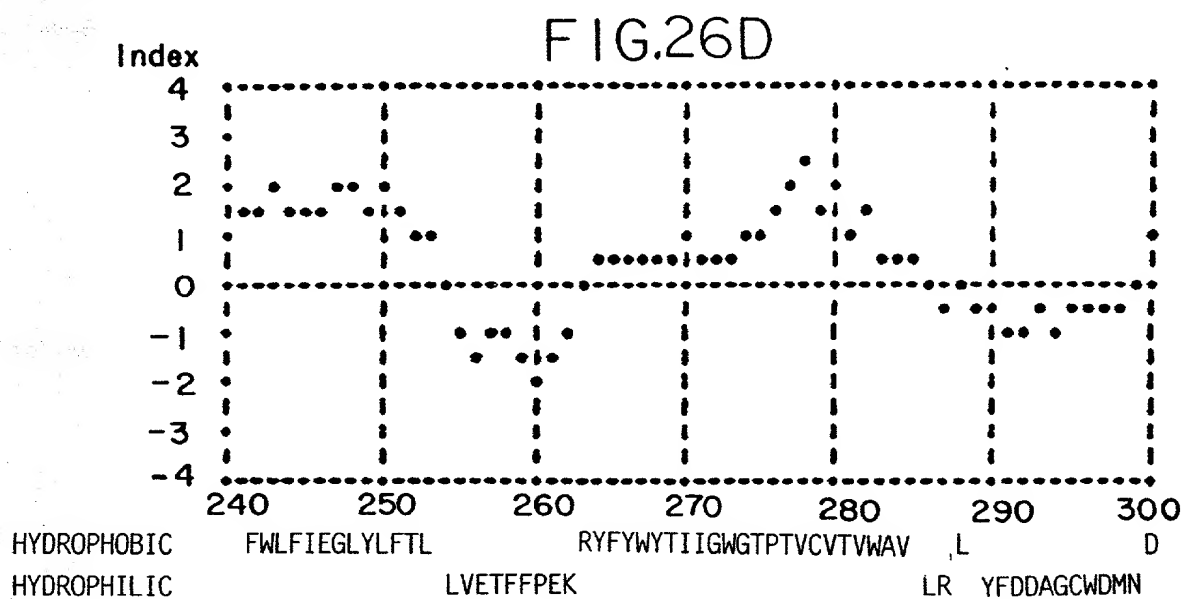
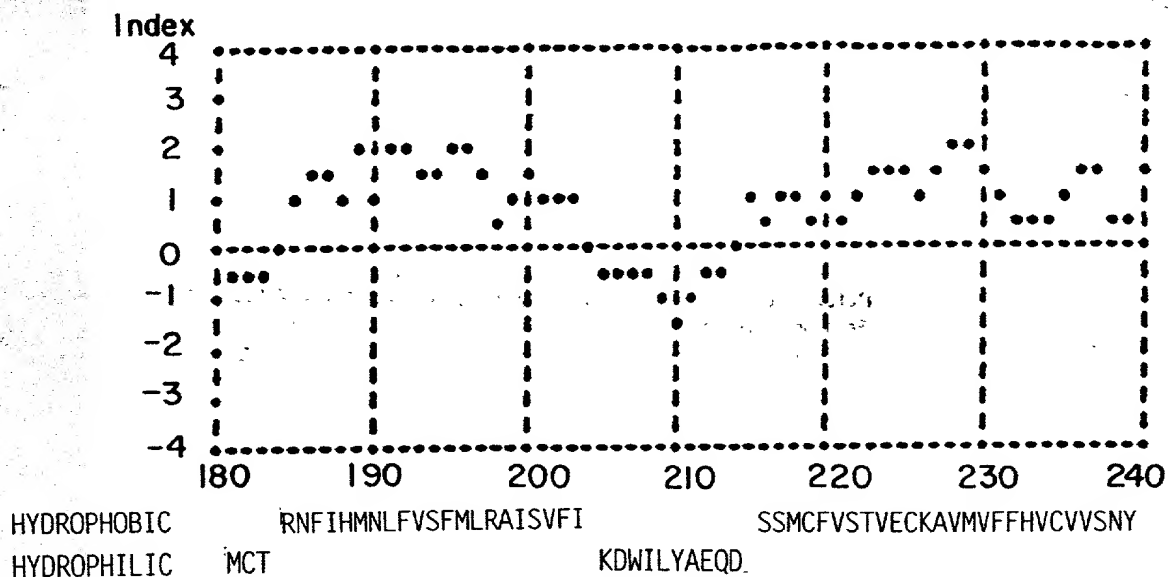
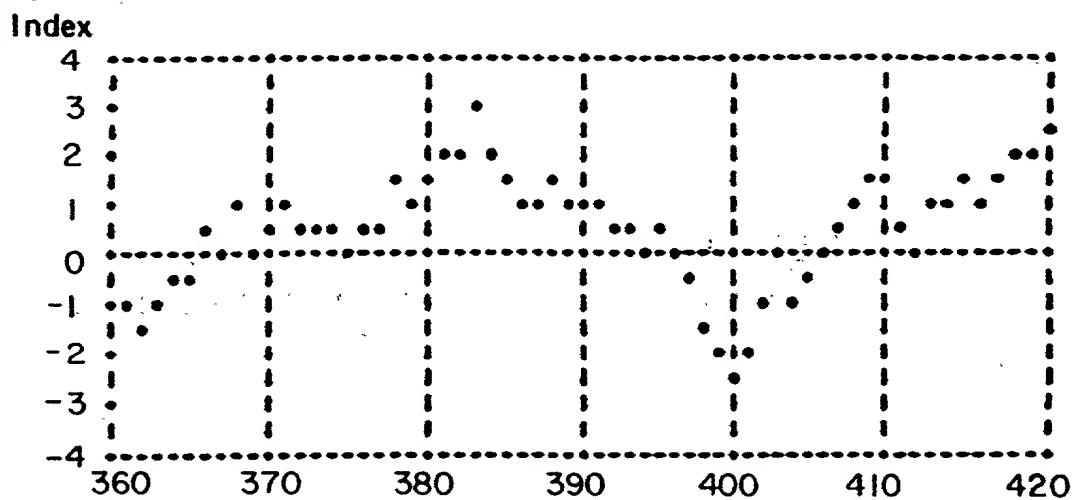
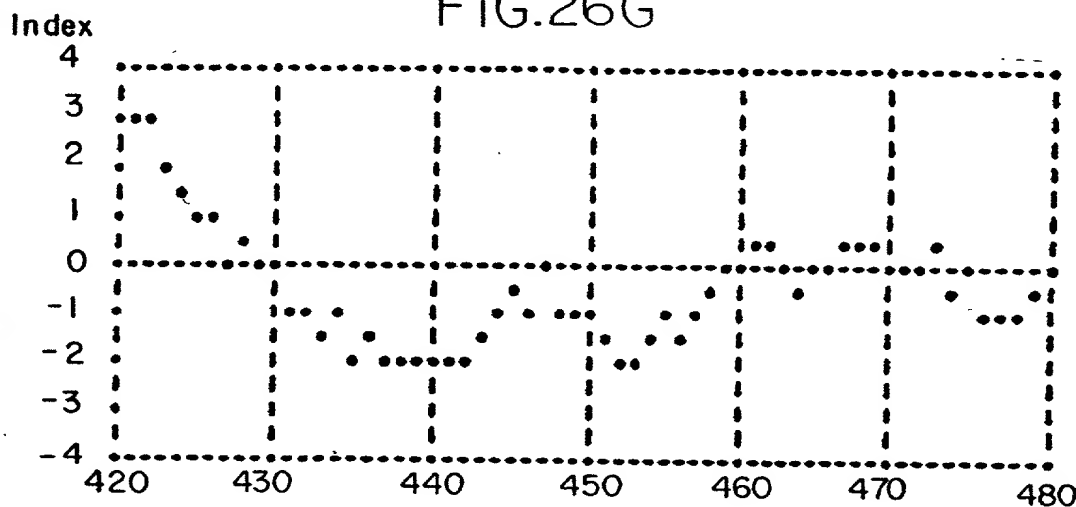


FIG. 26F



HYDROPHOBIC C MSELSTITRLARSTILLIPLFGIMYTVF ERLVFELGLGSFQG
 HYDROPHILIC AQQHS K. AFSPENVSKR

FIG.26G



HYDROPHOBIC FWVAVLYC MPSL VMGGTQL I
 HYDROPHILIC FLNGEVQAEIKRKWRSWKVNRYFTNDFEMR ASSG S LSRSS

FIG.26H

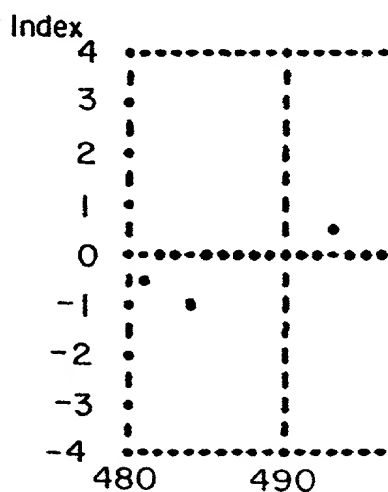


FIG.26I

HYDROPHOBIC QL MSSL NLA •
 HYDROPHILIC S R PAD T

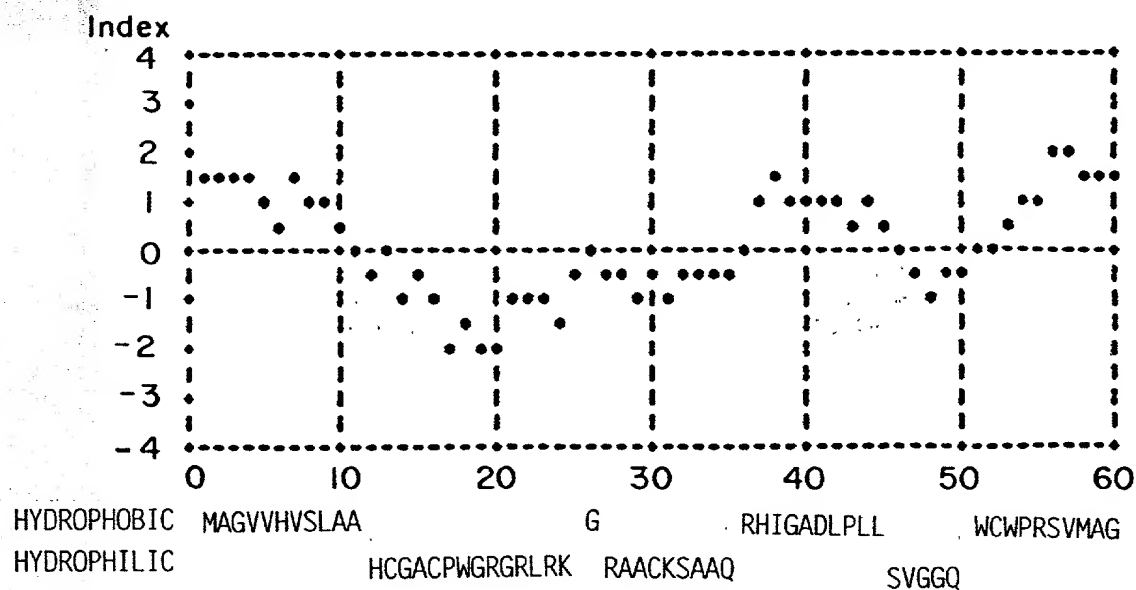


FIG.27A

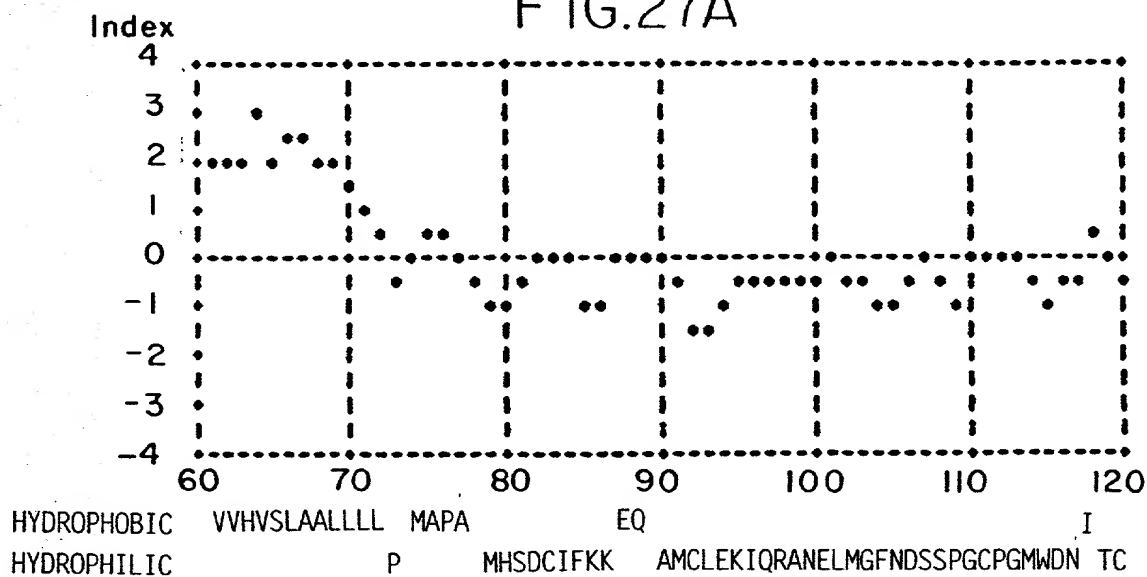


FIG.27B

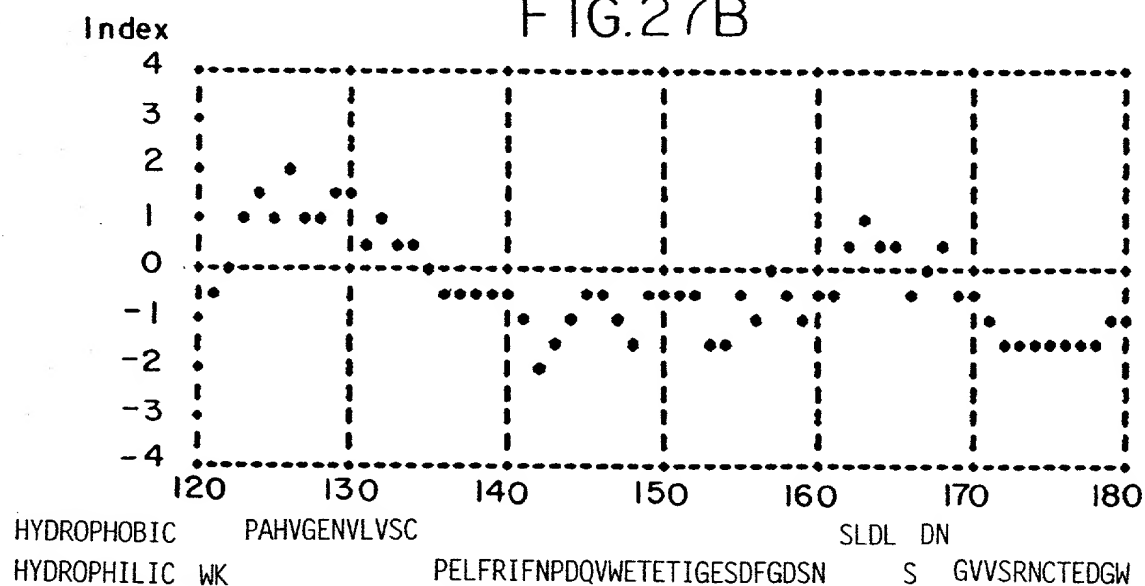


FIG.27C

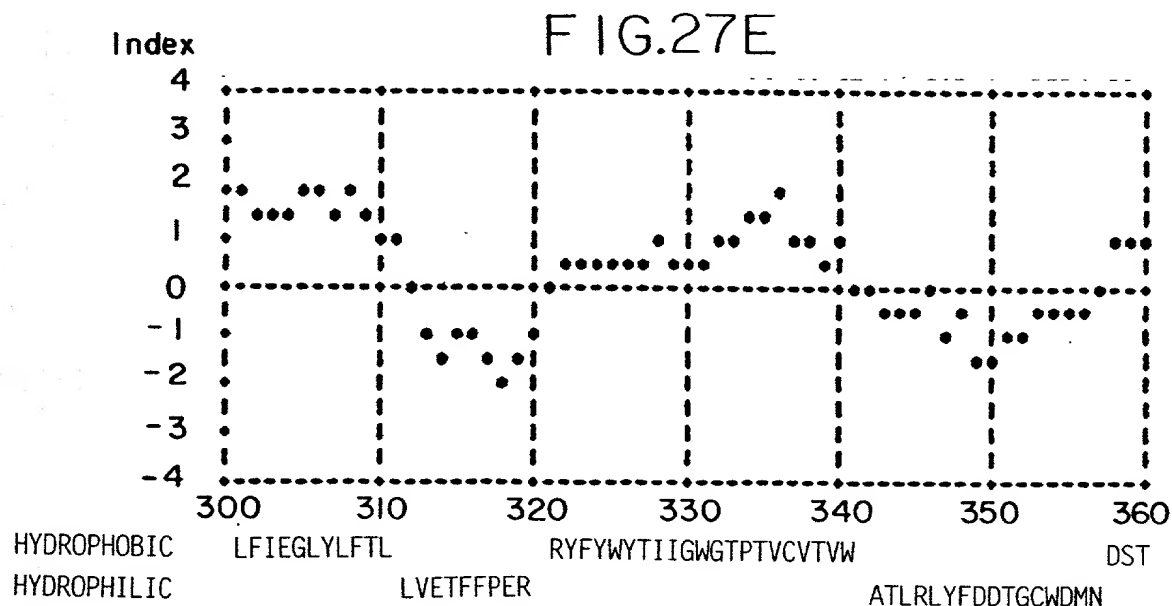
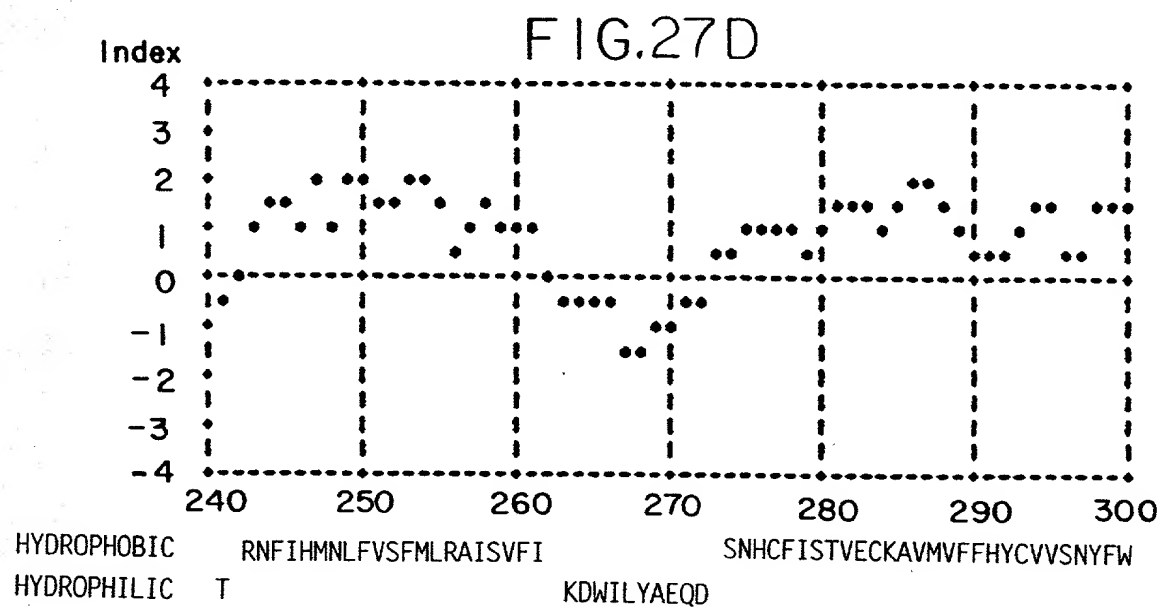
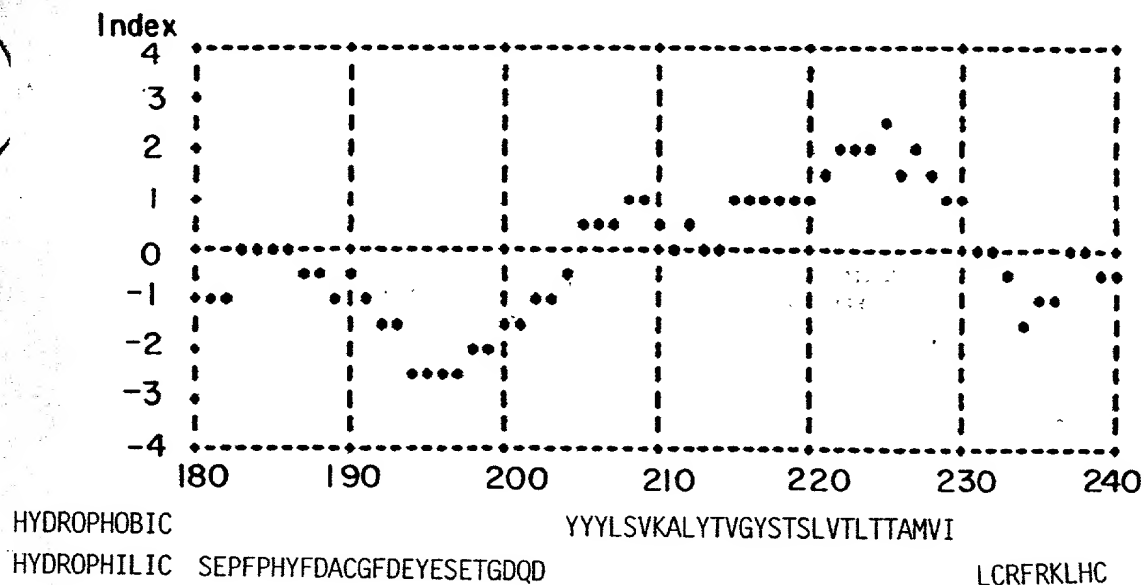


FIG.27F

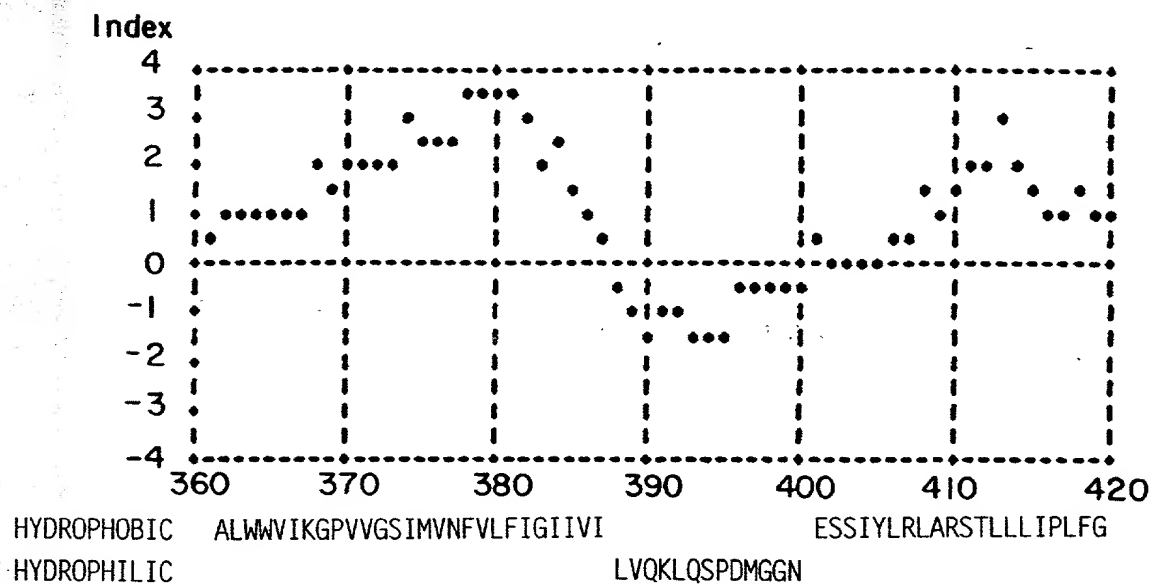


FIG. 27G

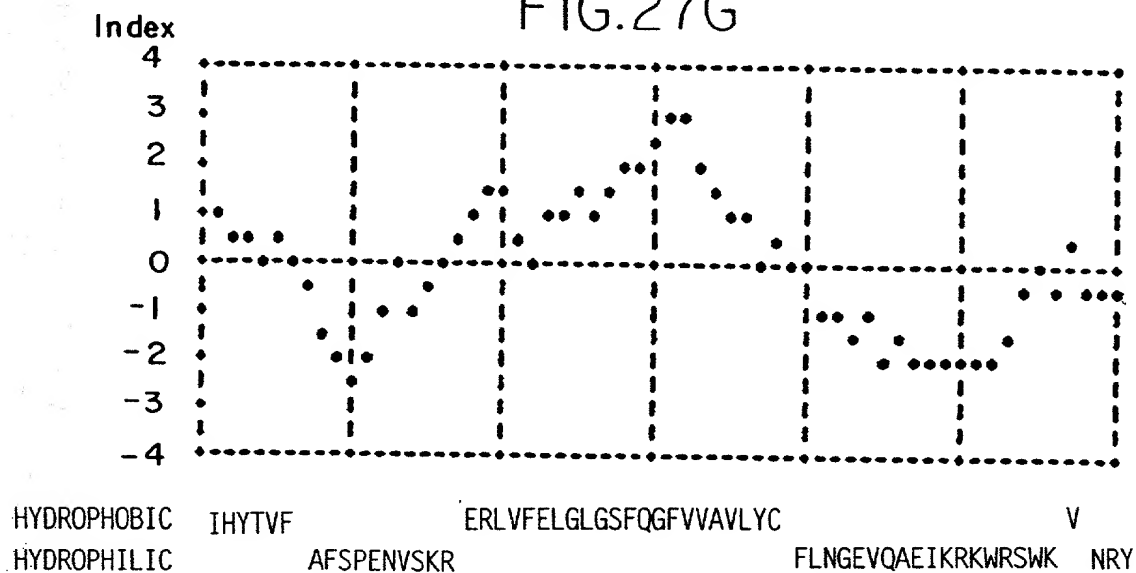
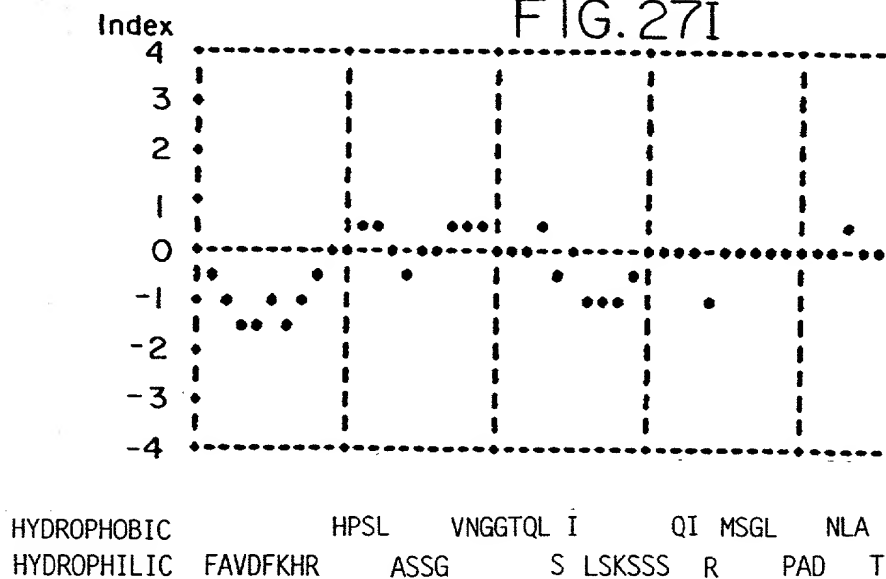


FIG. 27I



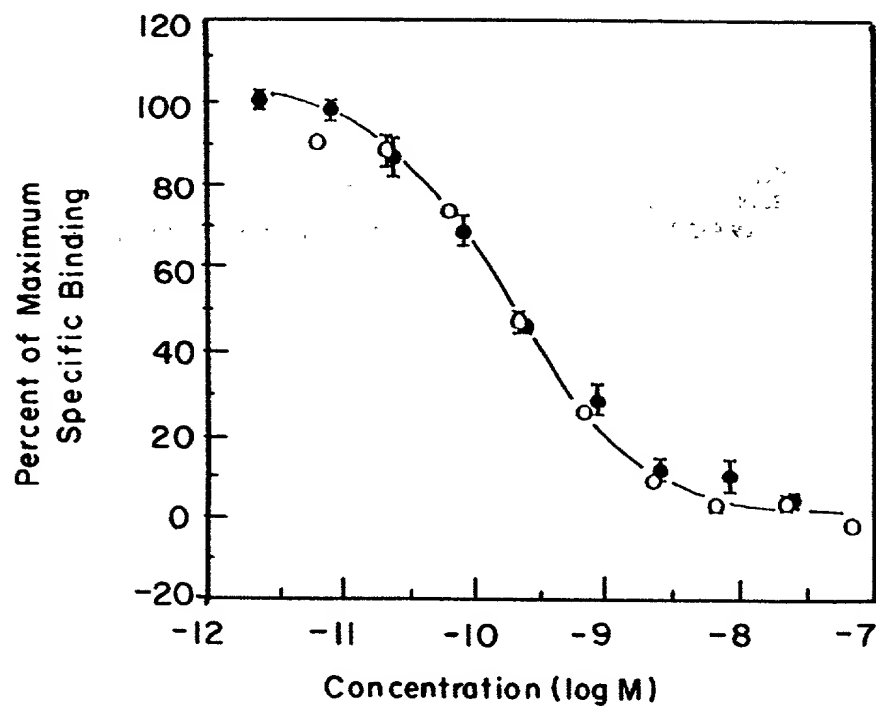


FIG. 29

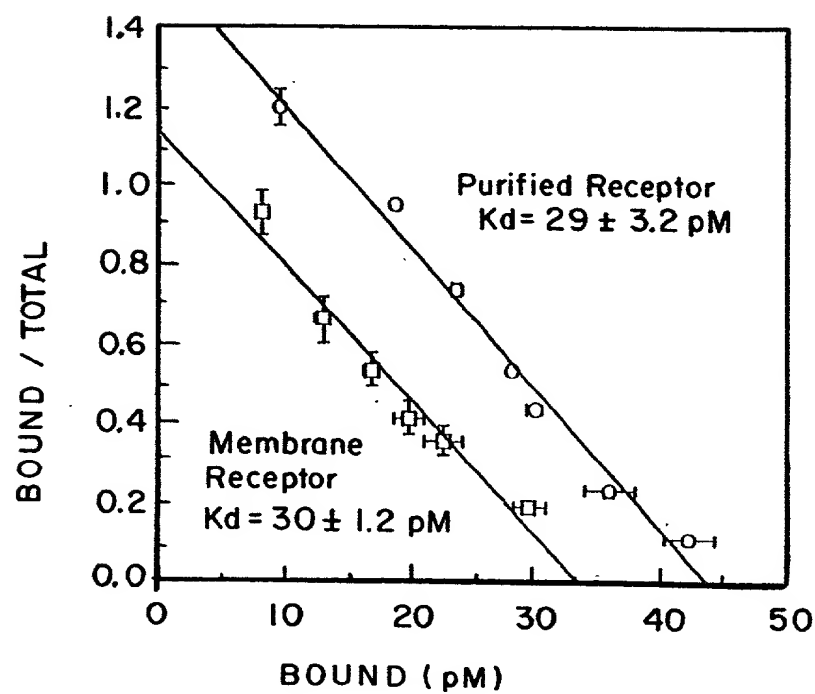


FIG. 30

FIG.31

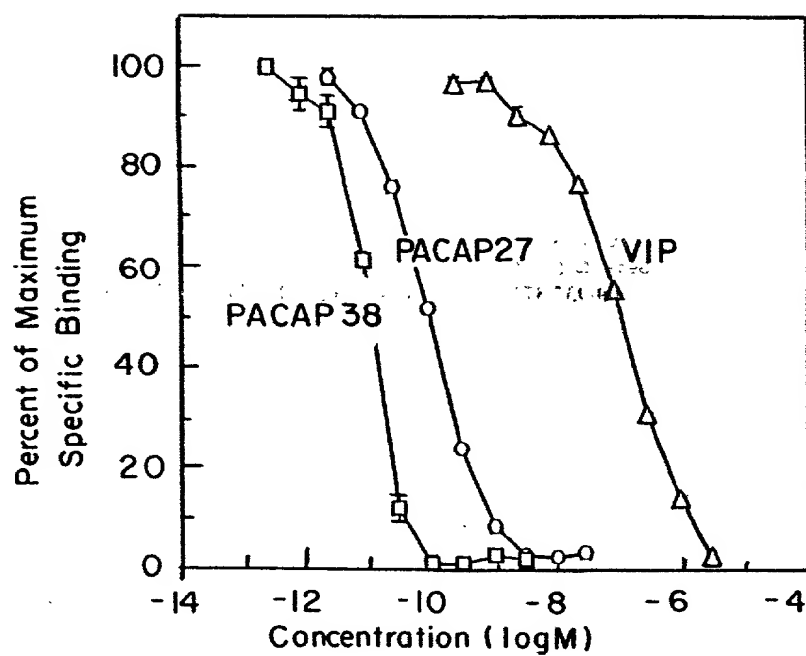


FIG.33

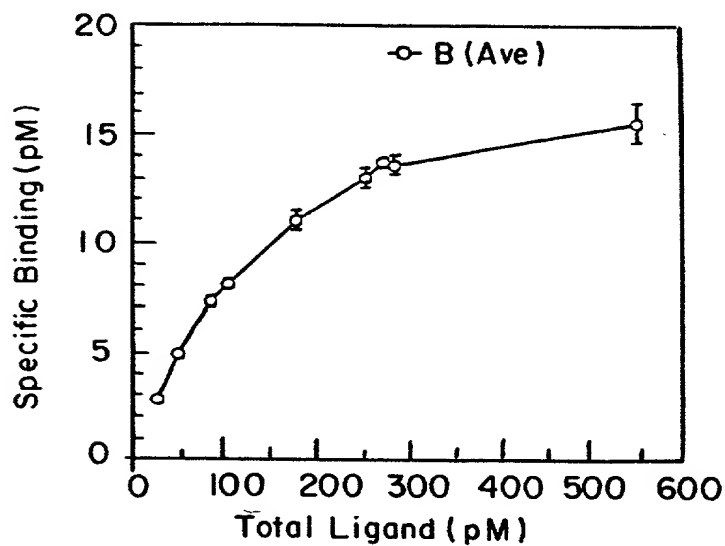


FIG.34

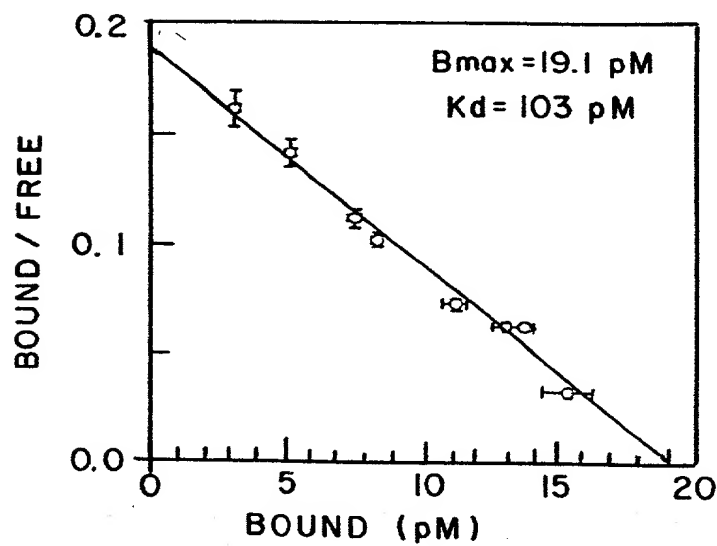


FIG. 35

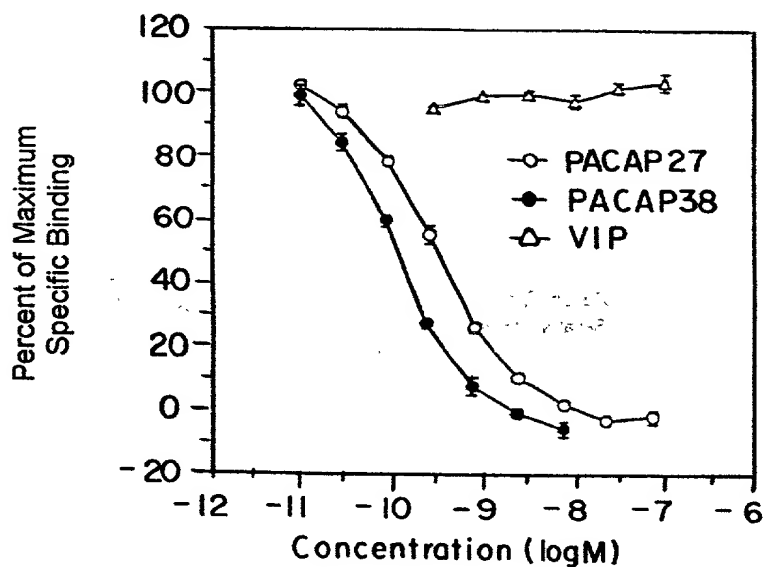


FIG.36

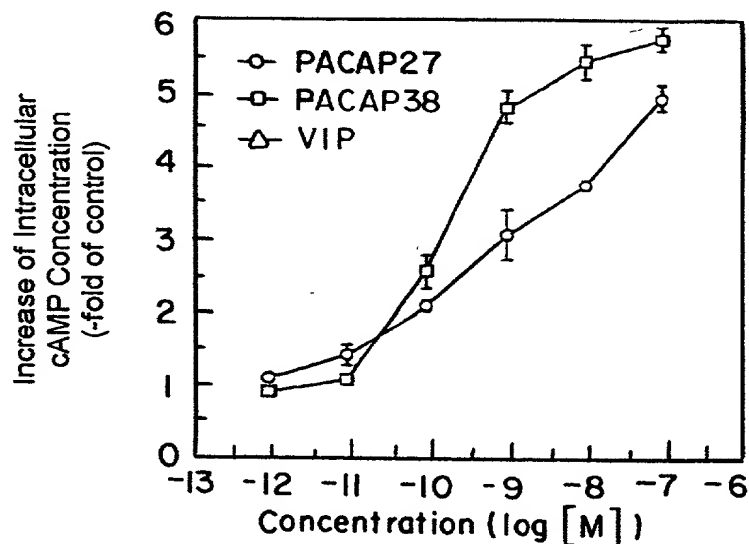


FIG.37

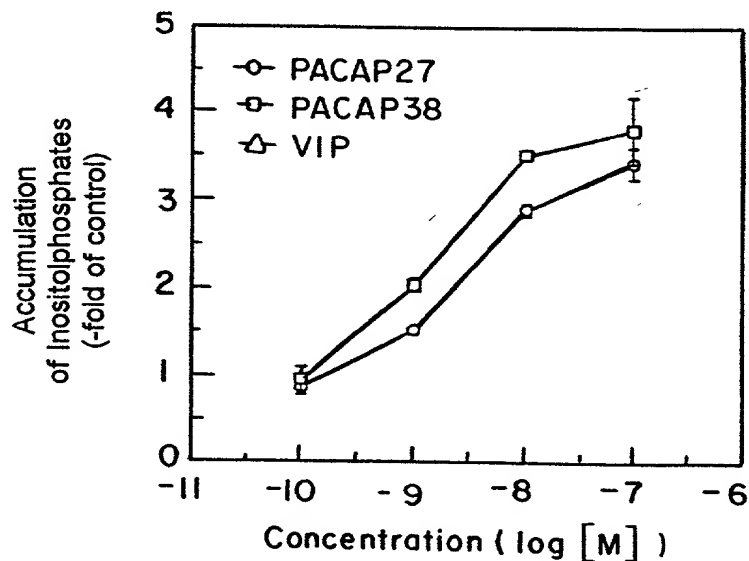


FIG.32

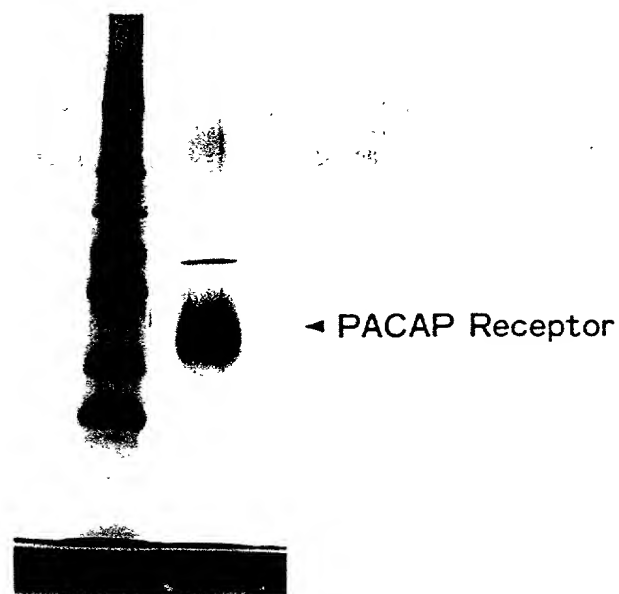


FIG.38

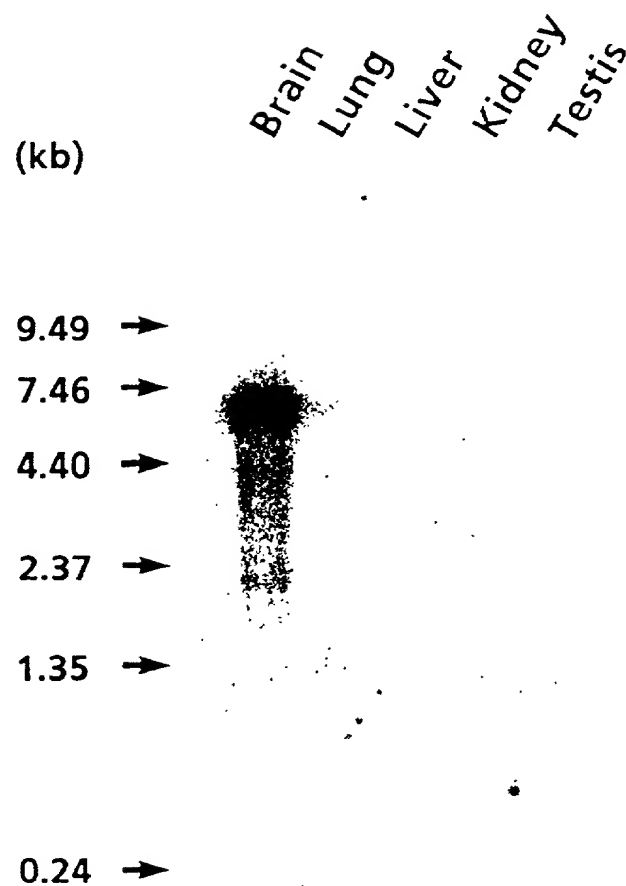


FIG.39

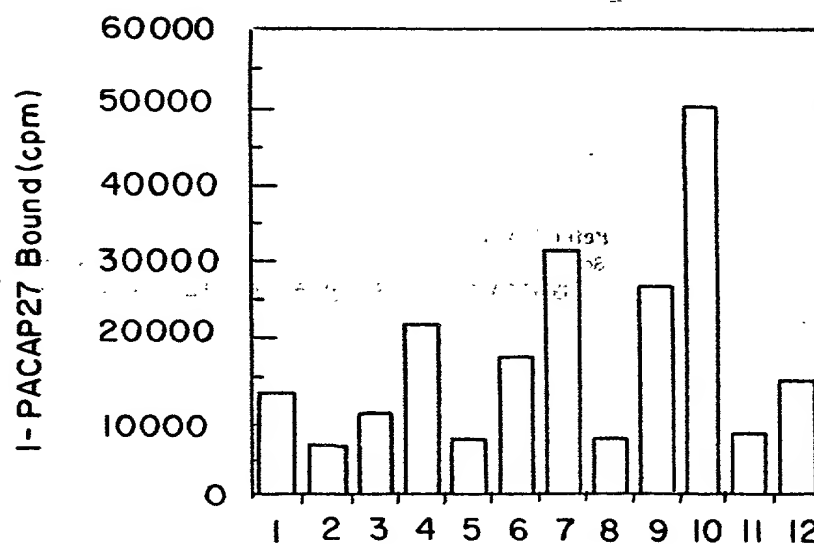


FIG.42

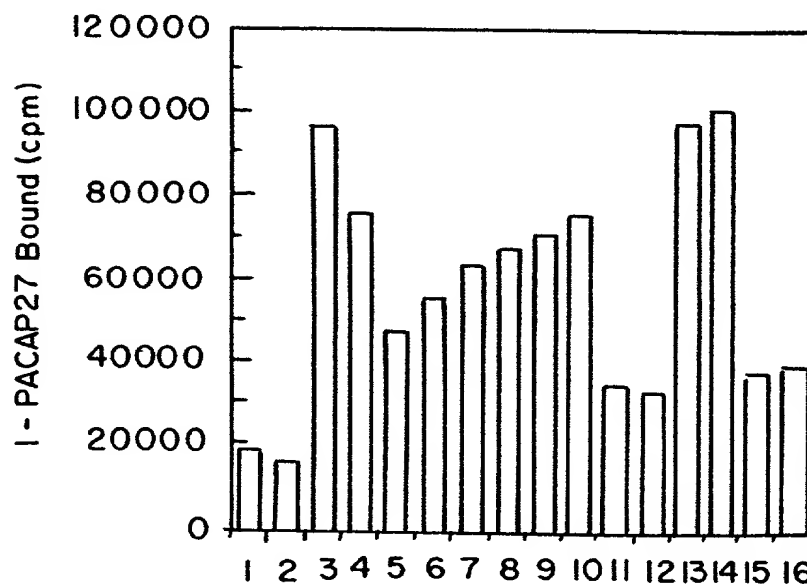
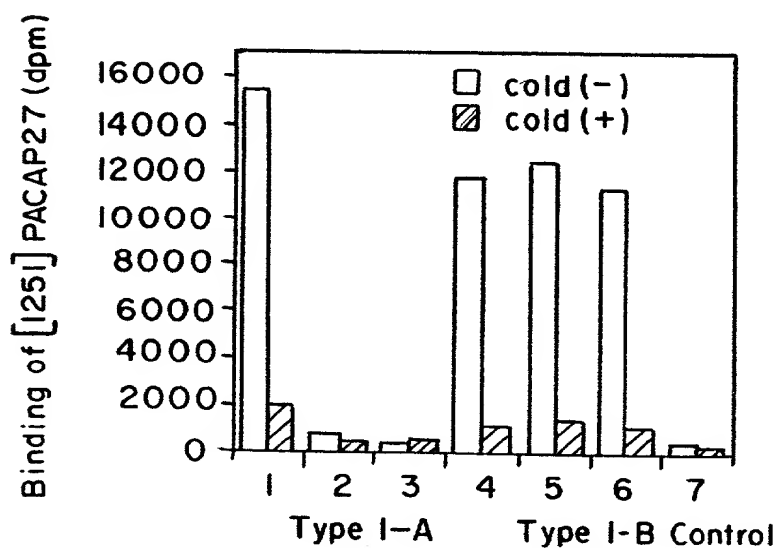


FIG.44



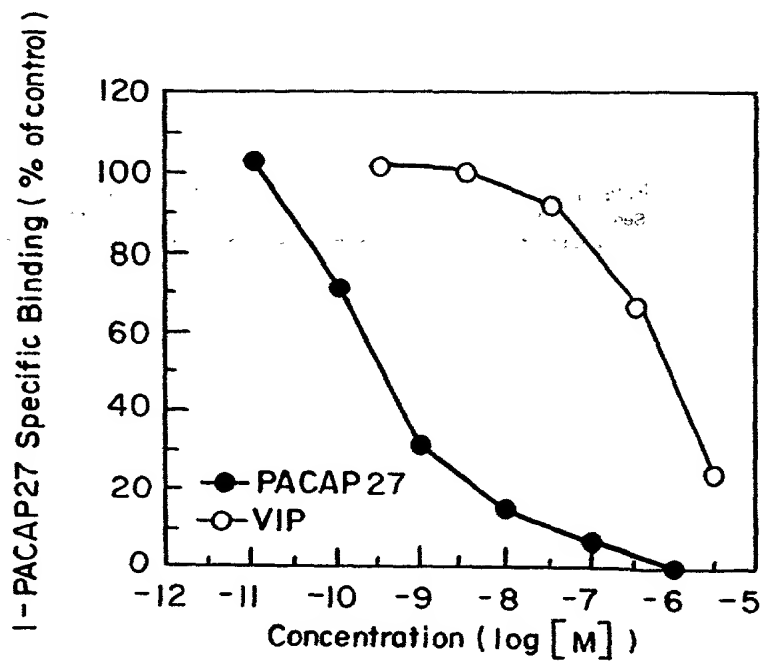


FIG. 40A

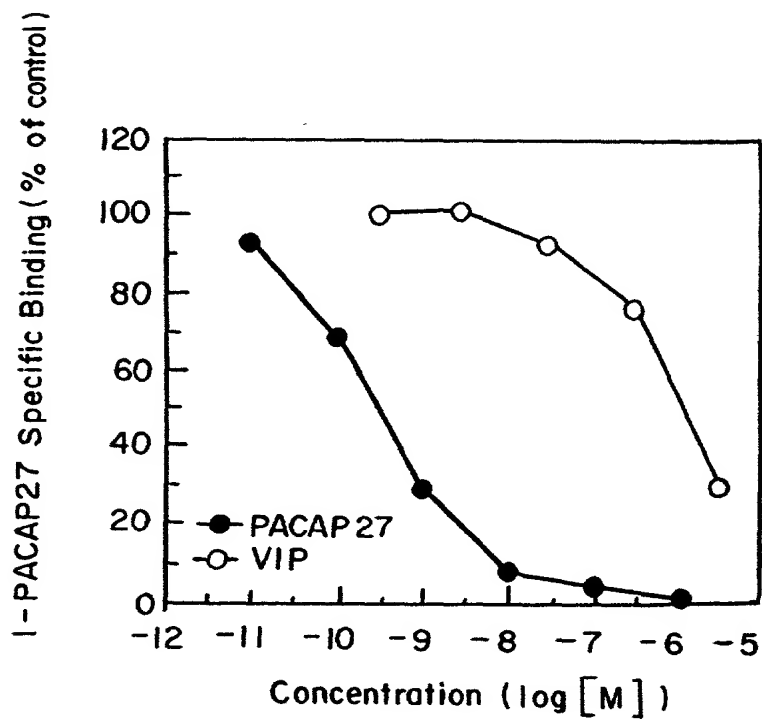


FIG. 40B

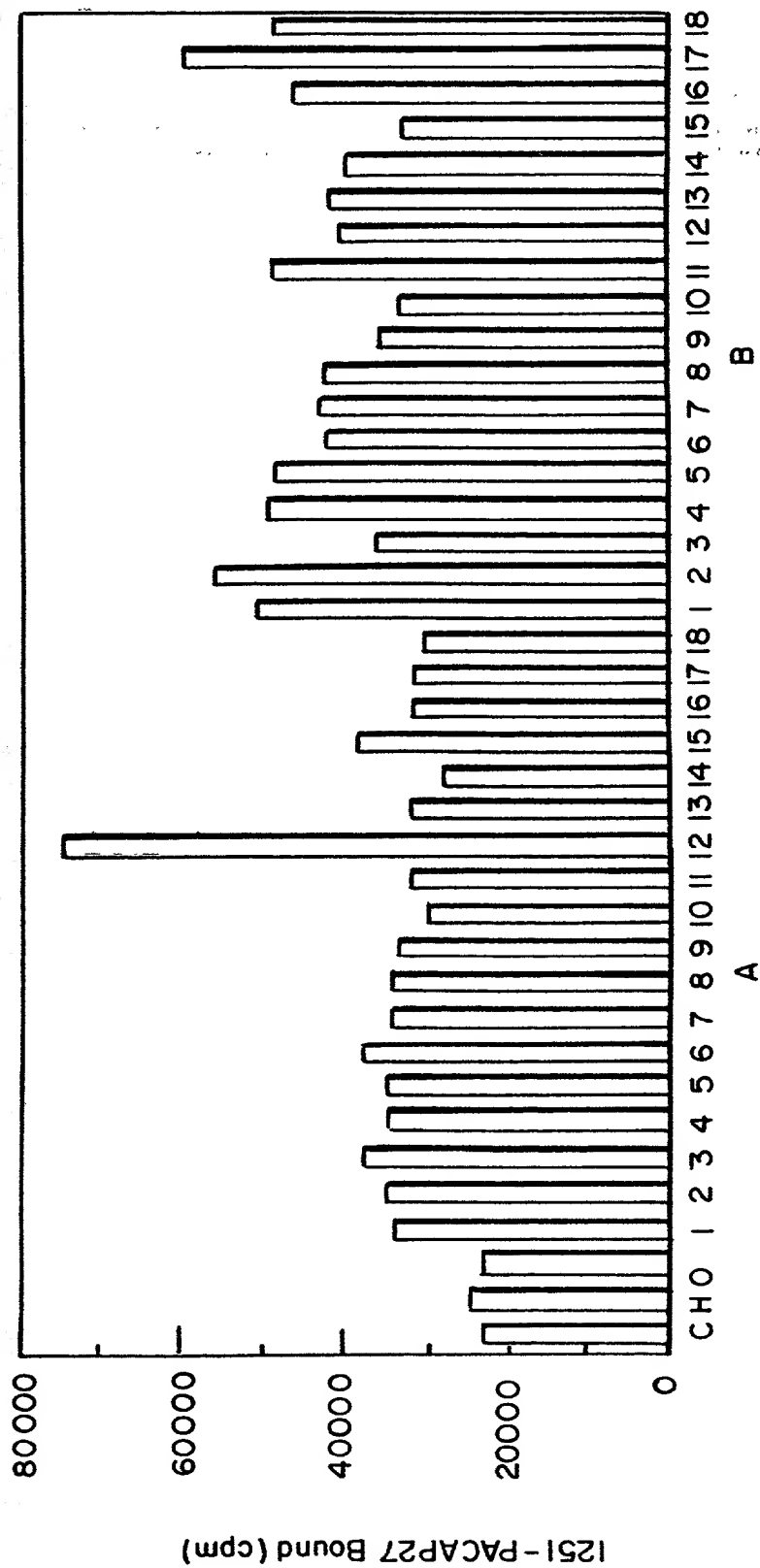


FIG. 41

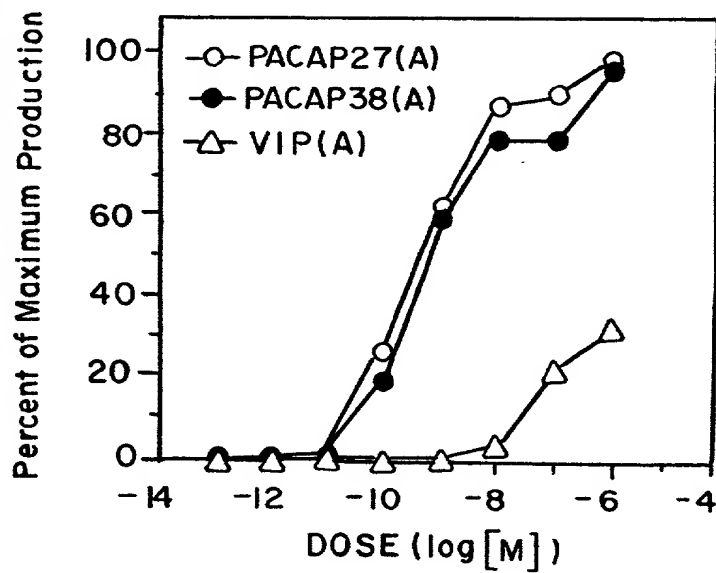


FIG. 43A

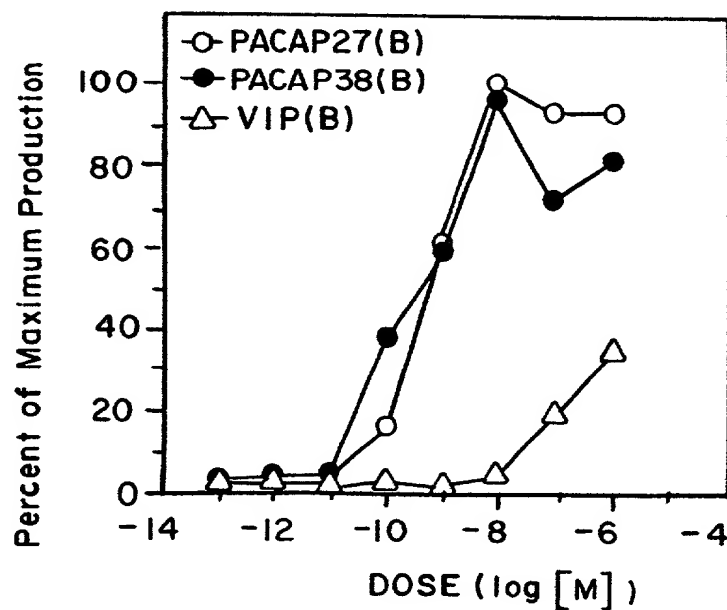


FIG. 43B

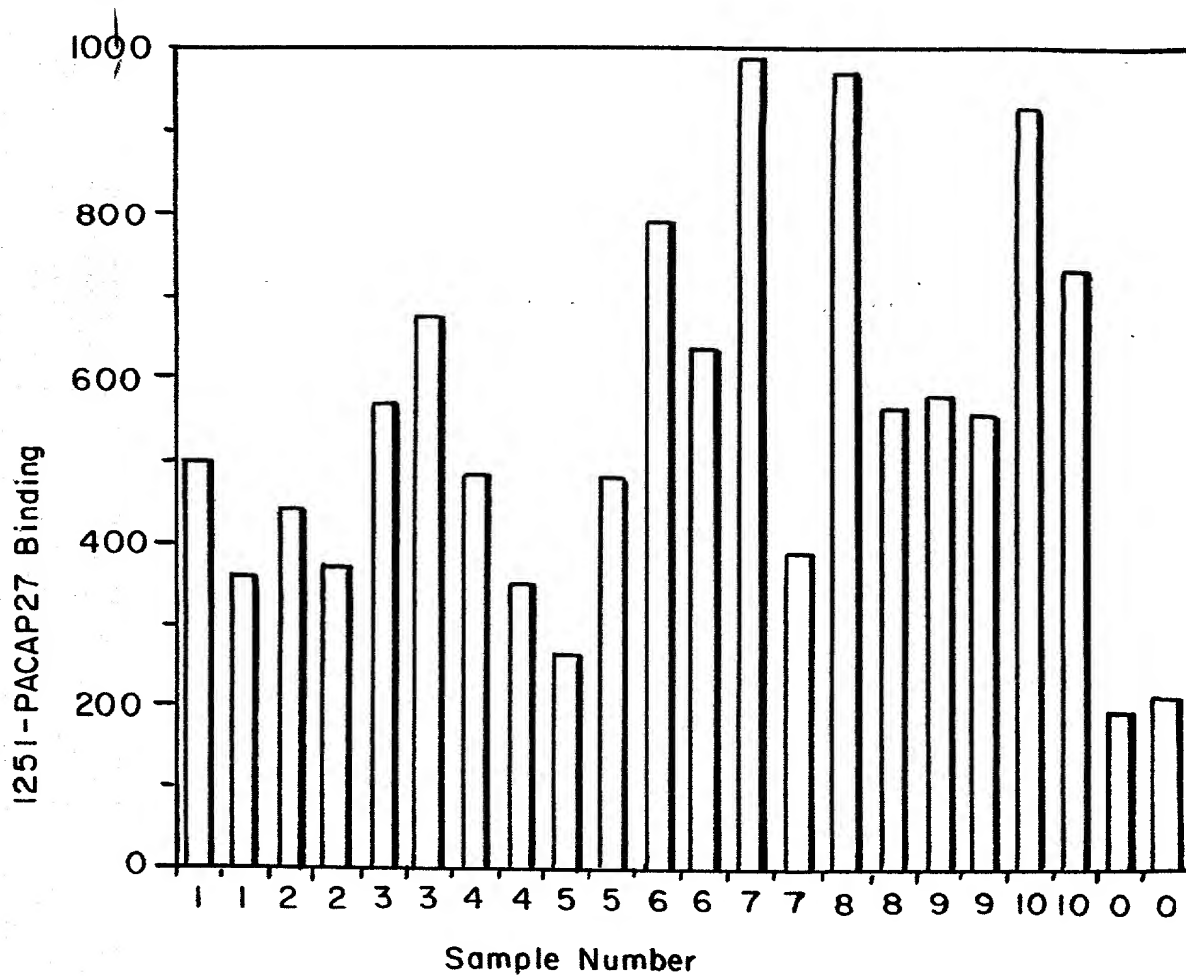


FIG. 45

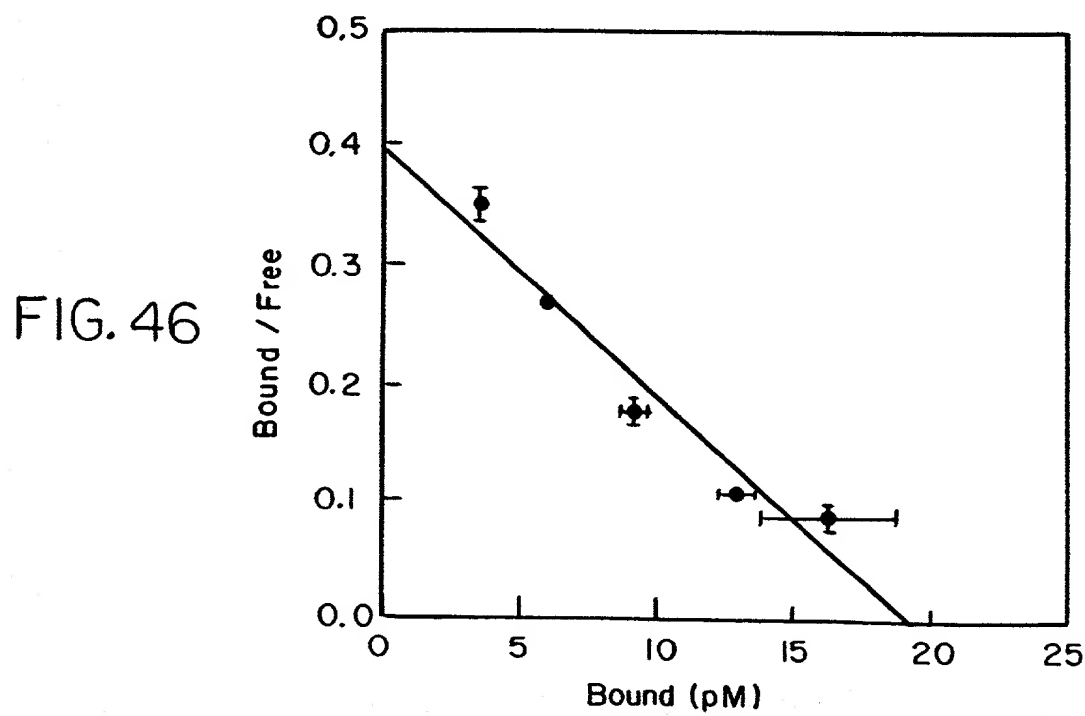


FIG.47

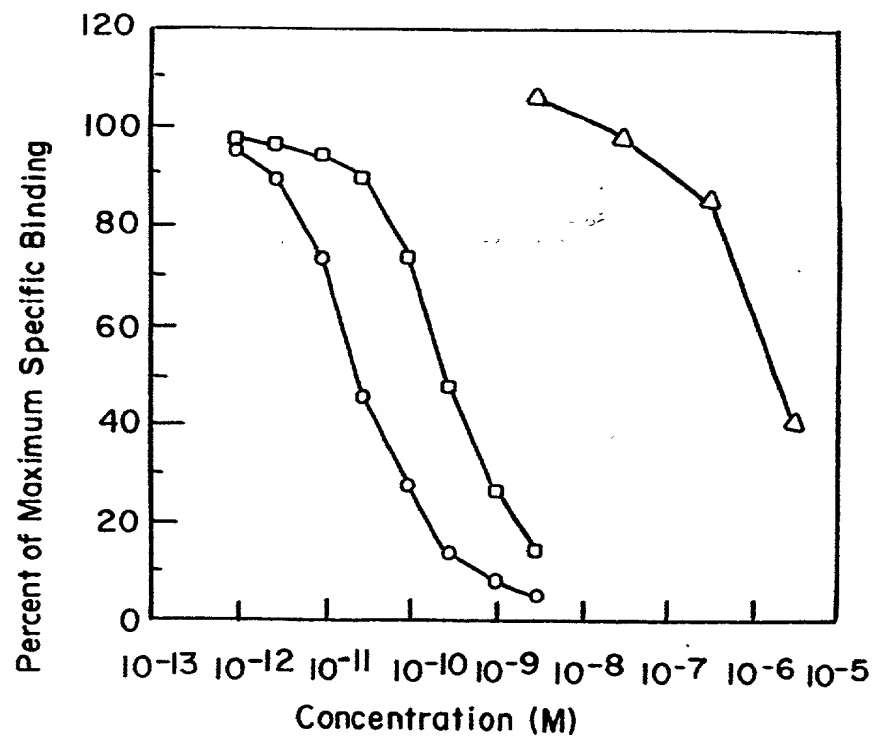
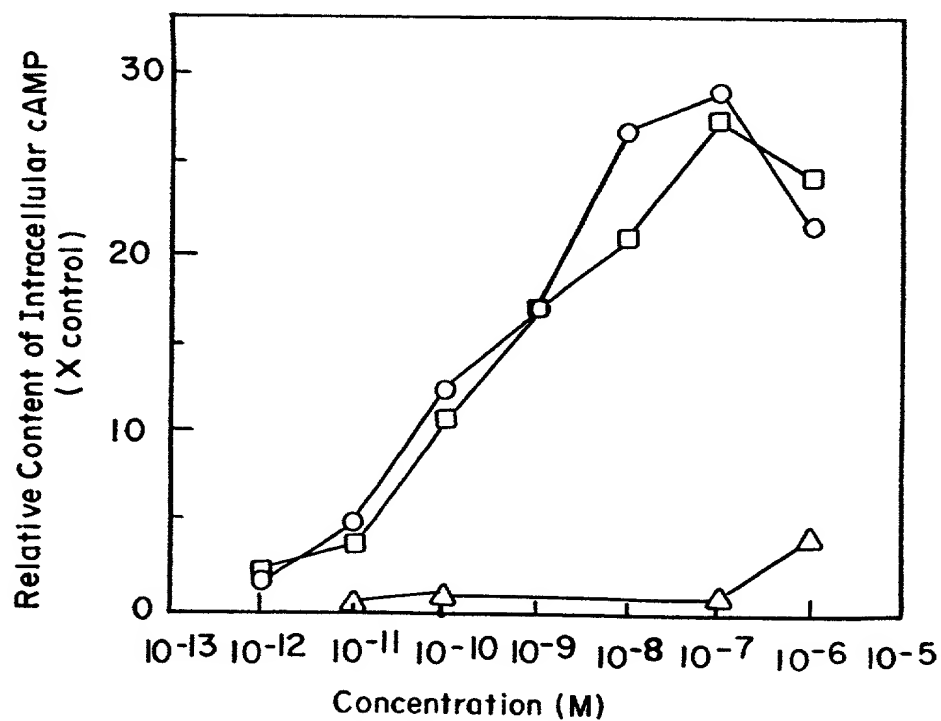


FIG.48



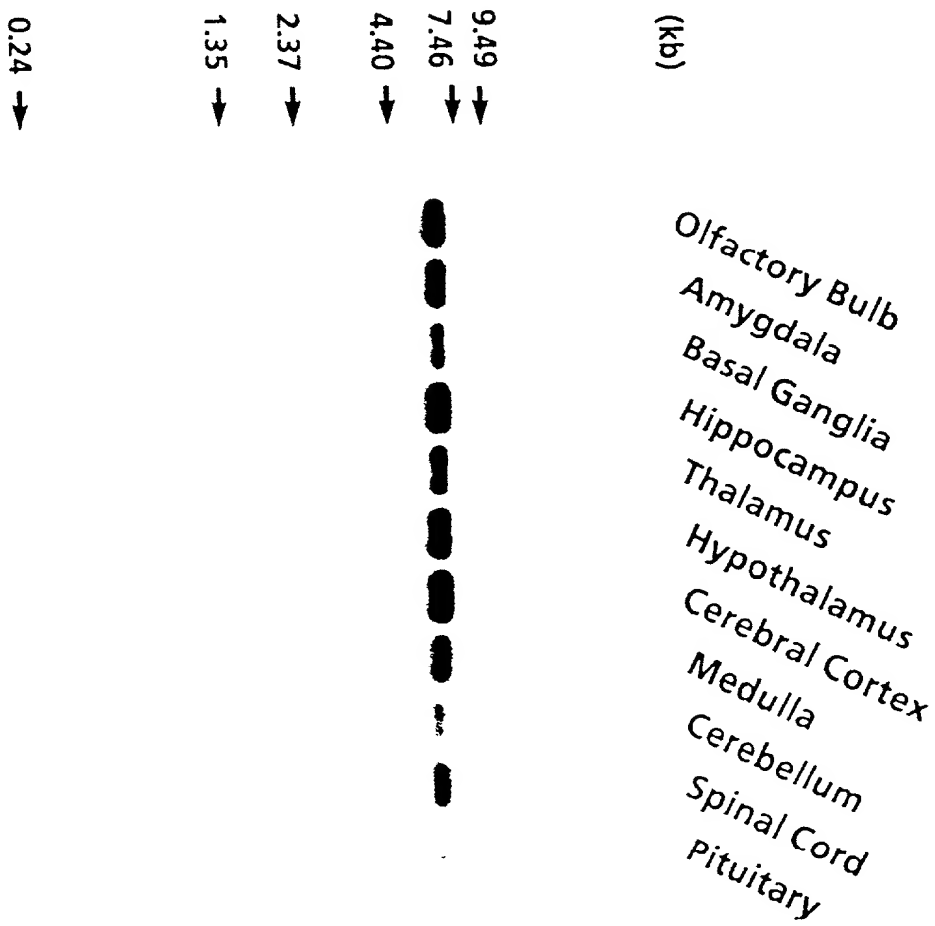
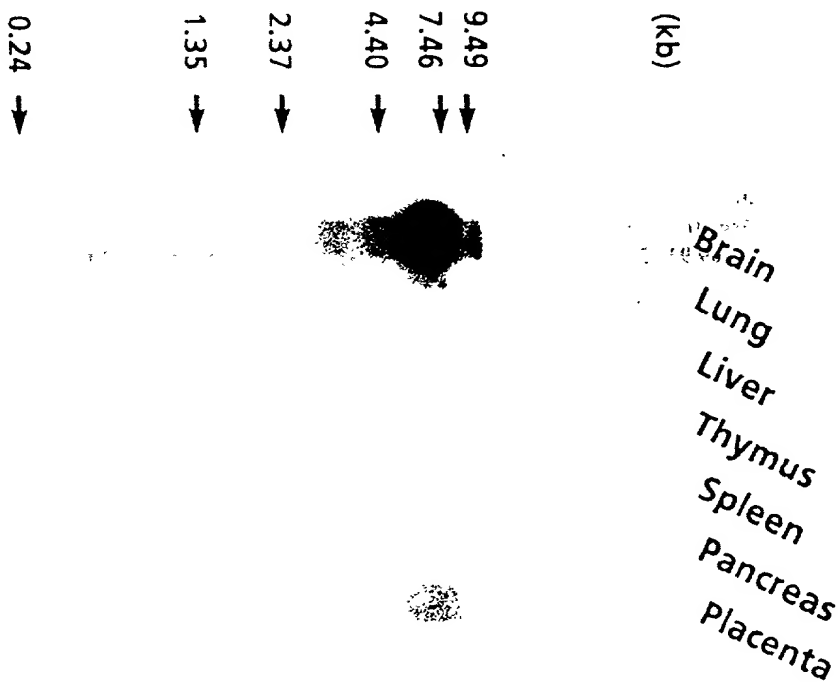


FIG. 49

FIG. 50

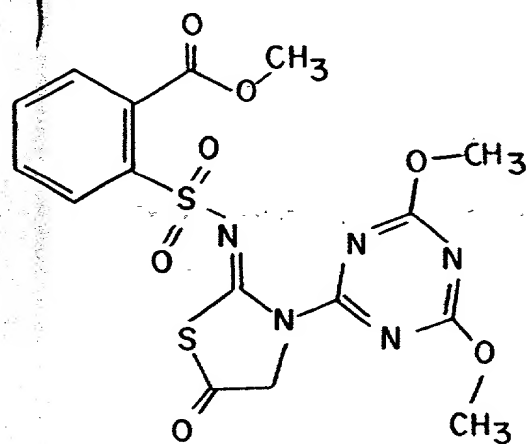


FIG. 5IA

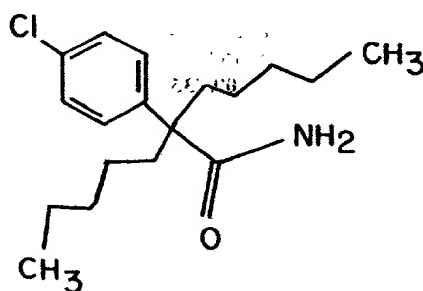


FIG. 5IB

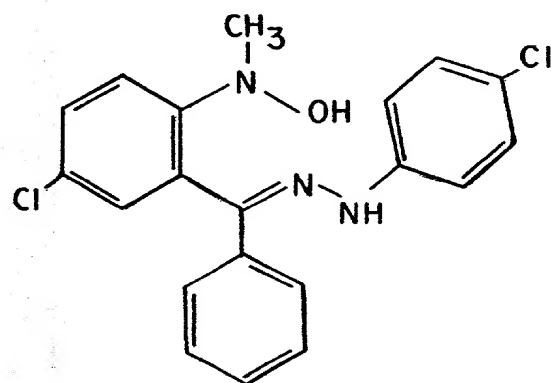


FIG. 5IC

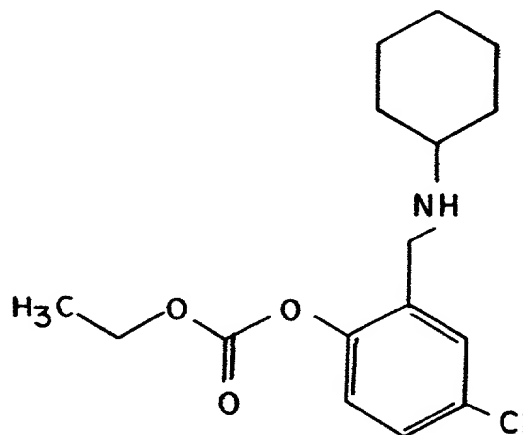


FIG. 5ID

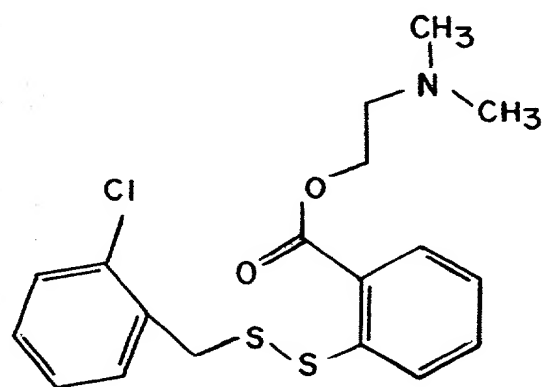


FIG. 5IE

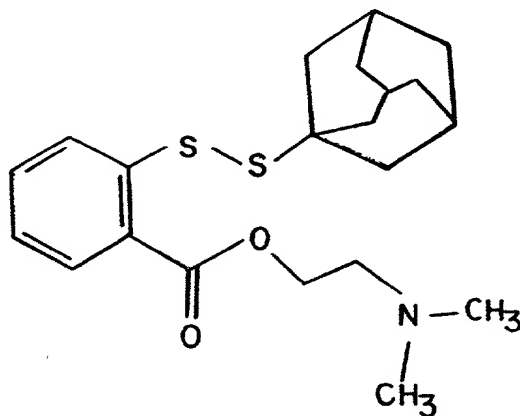


FIG. 5IF

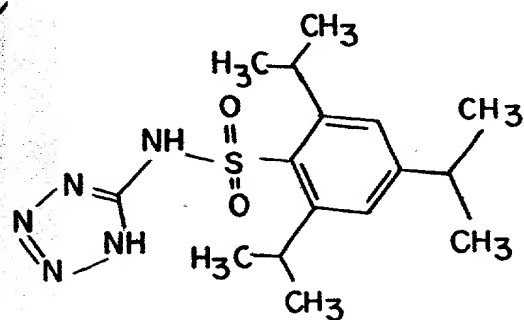


FIG. 5IG

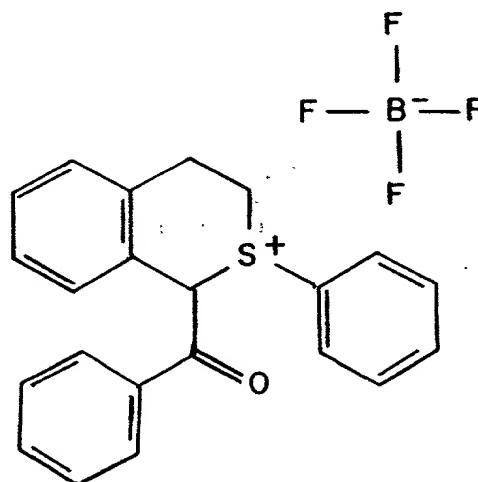


FIG. 5IH

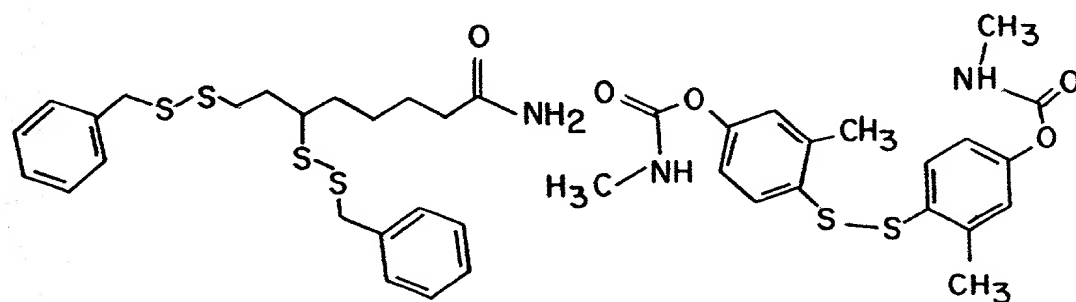


FIG. 5II

FIG. 5IJ

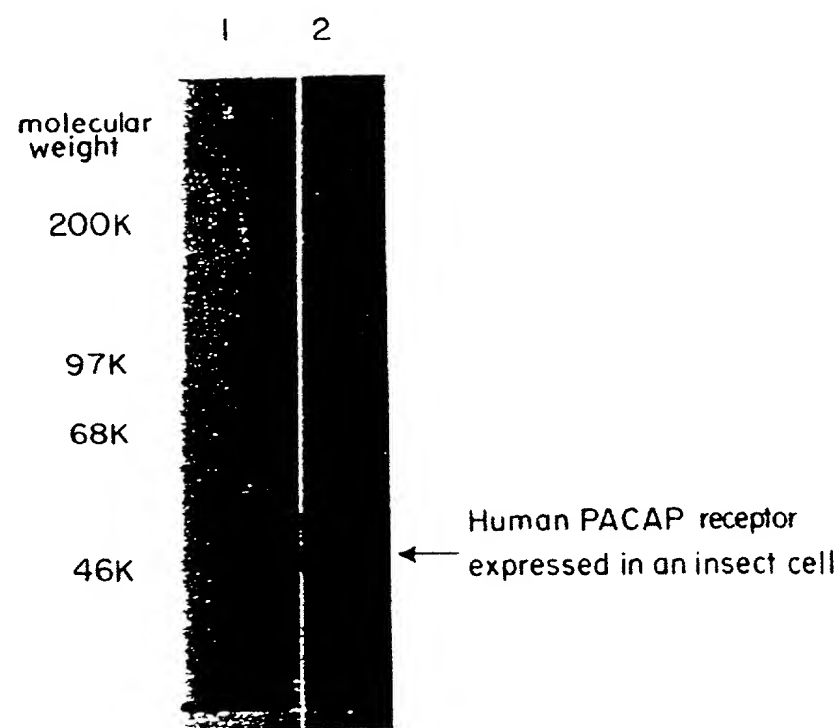


FIG. 53

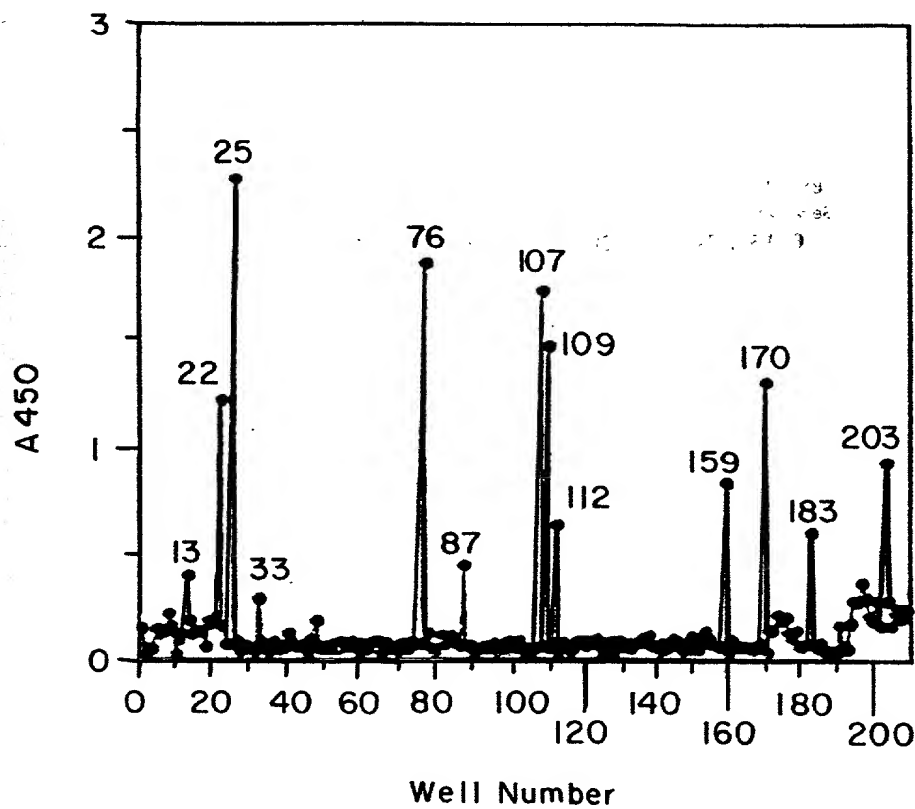


FIG. 52

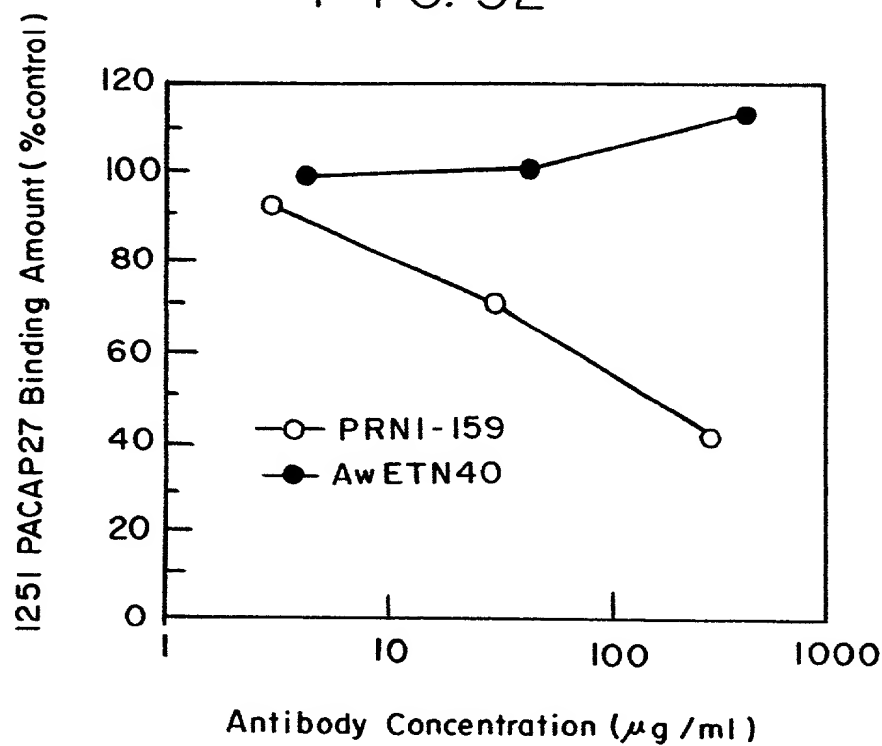


FIG. 54